

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:49:14 ; Search time 4394 Seconds
(without alignments)
10187.345 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_A146311

Perfect score: 700

Sequence: 1 ctgtttcacataaagttttt.....gcccttttagtgatggcga 700

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

GenEmbl.*

1: gb env.*

2: gb pat.*

3: gb ph.*

4: gb pl.*

5: gb pr.*

6: gb ro.*

7: gb sts.*

8: gb sv.*

9: gb un.*

10: gb vi.*

11: gb ov.*

12: gb hg.*

13: gb in.*

14: gb om.*

15: gb ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	698.4	99.8	127447	5	AC006344	AC006344 Homo sapi
c 2	168	24.0	197215	12	AC167793	AC167793 Bos tauru
c 3	115.6	16.5	159859	12	AC074010	AC074010 Homo sapi
4	115.6	16.5	172573	5	AC007276	AC007276 Homo sapi
5	115.2	16.5	147859	12	AC011079	AC011079 Homo sapi
6	115.2	16.5	169821	12	AC025490	AC025490 Homo sapi
c 7	115.2	16.5	186370	5	AC093671	AC093671 Homo sapi
8	115.2	16.5	212421	12	AC109591	AC109591 Homo sapi
9	114.4	16.3	161343	12	AC144869	AC144869 Pan trogl
10	114	16.3	135692	5	AC021134	AC021134 Homo sapi
11	114	16.3	156393	12	AC116177	AC116177 Homo sapi
12	113.2	16.2	154369	5	AC004803	AC004803 Homo sapi
13	113.2	16.2	157492	5	AC008836	AC008836 Homo sapi
c 14	112.8	16.1	66795	12	AC110584	AC110584 Homo sapi
15	112.8	16.1	191004	5	AC124649	AC124649 Homo sapi
16	112.8	16.1	207181	12	AC016756	AC016756 Homo sapi
17	112.8	16.1	210629	5	AC090150	AC090150 Homo sapi
c 18	112	16.0	157003	12	AC008022	AC008022 Homo sapi

19	112	16.0	166787	5	AC055723	AC055723 Homo sapi
c 20	112	16.0	183720	12	AC092912	AC092912 Homo sapi
21	112	16.0	186144	12	AC069048	AC069048 Homo sapi
c 22	111.6	15.9	601	7	BV184889	BV184889 squm14628
c 23	110.8	15.8	758	7	BV612024	BV612024 S217P6184
c 24	110.8	15.8	182301	5	AC012498	AC012498 Homo sapi
c 25	110.6	15.8	33223	5	AC009296	AC009296 Homo sapi
c 26	110.6	15.8	168624	5	AC092131	AC092131 Homo sapi
c 27	110.6	15.8	173189	5	AC092323	AC092323 Homo sapi
28	110.4	15.8	67307	12	AC120598_3	Continuation (4 of
29	110.4	15.8	110000	12	AC120598_2	Continuation (3 of
30	110.4	15.8	141677	5	AC114492	AC114492 Homo sapi
c 31	110.4	15.8	180247	12	AC053509	AC053509 Homo sapi
c 32	110.2	15.7	161297	5	AC146076	AC146076 Pan trogl
c 33	110.2	15.7	173479	5	AC097520	AC097520 Homo sapi
34	110.2	15.7	187017	12	AC112190	AC112190 Homo sapi
35	110.2	15.7	203278	5	AC010482	AC010482 Homo sapi
36	110.2	15.7	242730	12	AC099408	AC099408 Pan trogl
c 37	109.8	15.7	736	7	BV639424	BV639424 S217P6156
c 38	109.8	15.7	30936	5	AL672206	AL672206 Human DNA
c 39	109.6	15.7	58326	12	AC108383	AC108383 Pan trogl
c 40	109.6	15.7	5836	12	AC108384	AC108384 Pan trogl
c 41	109.4	15.6	45090	5	AL450486	AL450486 Human DNA
c 42	109.4	15.6	133458	12	AL137842	AL137842 Homo sapi
c 43	109.4	15.6	166793	12	AC090401	AC090401 Homo sapi
c 44	109.4	15.6	167934	5	AP001034	AP001034 Homo sapi
45	109.4	15.6	178544	5	AC007538	AC007538 Homo sapi
46	109.2	15.6	31105	5	AL158174	AL158174 Human DNA
c 47	109	15.6	144147	5	AC145394	AC145394 Pan trogl
c 48	109	15.6	146098	5	AC074112	AC074112 Homo sapi
49	109	15.6	181557	12	AC072055	AC072055 Homo sapi
50	109	15.6	186616	12	AC026294	AC026294 Homo sapi
51	108.8	15.5	139793	5	AC125629	AC125629 Homo sapi
52	108.6	15.5	107427	5	HS481A17	Z82212 Human DNA s
c 53	108.6	15.5	157075	5	AC005486	AC005486 Homo sapi
c 54	108.4	15.5	920	7	BV641191	BV641191 S215P6653
c 55	108	15.4	38837	12	AP006478	AP006478 Homo sapi
c 56	107.8	15.4	32196	5	AC110797	AC110797 Homo sapi
57	107.8	15.4	177219	12	AC021286	AC021286 Homo sapi
c 58	107.6	15.4	117409	5	AC008400	AC008400 Homo sapi
c 59	107.6	15.4	171808	12	AC141585	AC141585 Homo sapi
c 60	107.6	15.4	172875	5	AC084301	AC084301 Homo sapi
61	107.6	15.4	189812	5	AC009410	AC009410 Homo sapi
62	107.6	15.4	203171	5	AC108116	AC108116 Homo sapi
63	107.6	15.4	206589	5	AC009483	AC009483 Homo sapi
c 64	107.6	15.4	209434	5	AC026227	AC026227 Homo sapi
65	107.6	15.4	326786	12	AC022365	AC022365 Homo sapi
66	107.4	15.3	171832	5	AC079942	AC079942 Homo sapi
67	107.2	15.3	110000	12	AC079625_0	AC079625 Homo sapi
68	107.2	15.3	110000	12	AC018743_2	Continuation (3 of
69	107	15.3	58645	5	AC002068	AC002068 Homo sapi
c 70	107	15.3	139556	5	AC079943	AC079943 Homo sapi

ALIGNMENTS

RESULT 1	AC006344	127447 bp	DNA	linear	PRI 21-DEC-1999
AC006344/c	Homo sapiens PAC clone RP4-726N20	from 7q32-q34,	complete sequence.		
LOCUS	AC006344				
DEFINITION	Homo sapiens				
ACCESSION	AC006344.2	GI:4508150			
VERSION	HTG.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo				
REFERENCE	1 (bases 1 to 127447)				
AUTHORS	Sulston, J.E. and Waterston, R.				
TITLE	Toward a complete human genome sequence				
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)				

9847074
 2 (bases 1 to 127447)
 Cordes, M., Wohlman, P., Pape, K. and Horic, M.
 The sequence of Homo sapiens PAC clone RP4-726N20
 Unpublished
 3 (bases 1 to 127447)
 Waterston, R.H.
 Direct Submission
 Submitted (11-JAN-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 127447)
 Waterston, R.H.
 Direct Submission
 Submitted (24-MAR-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 127447)
 Waterston, R.
 Direct Submission
 Submitted (10-JUL-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 6 (bases 1 to 127447)
 Waterston, R.
 Direct Submission
 Submitted (21-DEC-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Mar 24, 1999 this sequence version replaced gi:4139379.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wuston.wustl.edu
 ----- Summary Statistics
 Center project name: H_DJ0726N20

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and
 sequencing collaboration between the NHGRI Chromosome 7 Mapping
 Project (Eric D. Green, Director), John D. McPherson in the
 Department of Genetics (Washington University), and the Washington
 University Genome Sequencing Center. For additional information
 about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/OTB/CHR7>, send
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 This clone was derived from human PAC library RPCI-4, prepared by
 Pieter de Jong and coworkers at the Roswell Park Cancer Institute
 (<http://bacpac.med.buffalo.edu>) using the method described by
 Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
 one male donor.
 The clone may be obtained either from Genome Systems, Inc.
 (<http://www.genomesystems.com>) or Research Genetics, Inc.
 (<http://www.resgen.com>); or from Pieter de Jong.
 VECTOR: pCYPAC2
 NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP4-529P3. Actual start of this
 clone is at base position 1 of RP4-726N20; actual end is at 127447

of RP4-726N20.
 The run of A's from 48936 to 48936 may contain one less A, no read
 was able to make an exact call.

FEATURES
 source
 1..127447
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="7"
 /map="7q32-q34"
 /clone="RP4-726N20"
 /clone_lib="RPCI-4"
 1..47
 /rpt_family="Alu"
 repeat_region
 48..72
 /rpt_family="Alu"
 repeat_region
 442..598
 /rpt_family="MIR1_type"
 repeat_region
 895..1086
 /rpt_family="MIR"
 repeat_region
 1873..1929
 /rpt_family="L1"
 repeat_region
 1932..2231
 /rpt_family="Alu"
 repeat_region
 3021..3035
 /rpt_family="Alu"
 repeat_region
 3036..3344
 /rpt_family="Alu"
 repeat_region
 3345..3509
 /rpt_family="Alu"
 repeat_region
 3754..4007
 /notes="match to EST AA102351 (NID:gl647100) z191c01.r1"
 misc_feature
 3754..4006
 /notes="similar to Mus musculus EST AA617614 (NID:g2504819)
 vi78g01.r1"
 gene
 <3755..11568
 /genes="WUGSC:H_DJ0726N20.1"
 CDS
 join(<3755..4006,6362..6490,7525..7578,11428..11568)
 /genes="WUGSC:H_DJ0726N20.1"
 /inference="non-experimental evidence, no additional
 details recorded"
 /notes="verified by mouse ESTs AA617614 (NID:g2504819) and
 AA237696 (NID:gl861718); H_DJ0726N20.1"
 /codon_start=1
 /protein_id="AAD43192.1"
 /db_xref="GI:5441947"
 /translation="IFVDNFVHADLHPGNILVQGANGLSSQEAQLQQAQADICDTLVVA
 VPSSLCPLRLVLLDAGIVAELOAPDLRNFRAVMVVGQQRVAELILHARASECR
 DVEGPKTENAMLVTOARKXTITLEKLHVSSLLSSVFKLLMTHKVKLESNFASIVFAIM
 VLEGGRSLDPKLDILEAARPLLITGPVCP"
 misc_feature
 3858..4006
 /genes="WUGSC:H_DJ0726N20.1"
 /notes="match to EST R62790 (NID:g834669) y110h10.r1"
 misc_feature
 3957..4006
 /genes="WUGSC:H_DJ0726N20.1"
 /notes="match to EST R55707 (NID:g825002) y988h12.s1"
 misc_feature
 3960..4006
 /genes="WUGSC:H_DJ0726N20.1"
 /notes="similar to EST R55994 (NID:g826100) y992b09.s1"
 repeat_region
 4069..4197
 /rpt_family="Alu"
 repeat_region
 4198..4496
 /rpt_family="Alu"
 repeat_region
 4497..4637
 /rpt_family="Alu"
 repeat_region
 4640..4763
 /rpt_family="Alu"
 repeat_region
 4814..5108
 /rpt_family="Alu"
 misc_feature
 4836..5222
 /genes="WUGSC:H_DJ0726N20.1"
 /notes="match to EST AA482844 (NID:g2211689) nf49a07.s1"

Qy	421	TAATTTGATTTTACCAAAATTTCCATGTGAAACAAACAGAGTTGGCTATTTTTTGGATTGATAT	480
Db	95109	TAATTTGATTTTACCAAAATTTCCATGTGAAACAAACAGAGTTGGCTATTTTTTGGATTGATAT	95050
Qy	481	TTTGAATAACTAGTACAGGAATATCATCTGTAGTTGAAATTTTTTTCAGCTTTAGAAAAACAAT	540
Db	95049	TTTGAATAACTAGTACAGGAATATCATCTGTAGTTGAAATTTTTTTCAGCTTTAGAAAAACAAT	94990
Qy	541	GGAGTTTTCATGCTAAAGTATAAATTTATTTGTTGATTTTAATATGCTATGGAGTTAGGCG	600
Db	94989	GGAGTTTTCATGCTAAAGTATAAATTTATTTGTTGATTTTAATATGCTATGGAGTTAGGCG	94930
Qy	601	TATGATAAATTTAGTGAACCAACCCAGAAATGTTTTTATCTTTTAAATTTTAAAAATTTGAAA	660
Db	94929	TATGATAAATTTAGTGAACCAACCCAGAAATGTTTTTATCTTTTAAATTTTAAAAATTTGAAA	94870
Qy	661	TGACACTTCGAGTAACAAATTCCTTTAGGTGATGGCA	700
Db	94869	TGACACTTCGAGTAACAAATTCCTTTAGGTGATGGCA	94830
RESULT 2			
AC167793/c			
LOCUS	Bos taurus clone CH240-216G5, WORKING DRAFT SEQUENCE, 8 unordered	197215 bp	DNA linear HTG 23-JAN-2006
DEFINITION	pieces.		
ACCESSION	AC167793		
VERSION	AC167793.2	GI:856664410	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	Bos taurus (cattle)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 197215)		
	Muzny,D., Adams,C., Agbai I.I., Allen,C., Alsbrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I., Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K., Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T., Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D., Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeblerlein,K., Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P., Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J., Hines,S., Hitchens,M., Hodgson,A., Hogues,M., Hollins,B., Howell,L.T., Hulyk,S., Hume,J., Imo,K., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kafafus,K., Kelly,S., Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F., Leal,S., Lee,K., Lee,S., LeCalle,F.I., Lemon,S., Lewis,L., Li,B., Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorensuhea,L., Lozano,R., Luk,T., Madu,R., Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E., McClelland,H., McPherson,J., Mercadao,C., Metzker,M., Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Munidasa,M., Murray,D., Nazareth,L., Ngo,D., Nguyen,N., Norwig-Eastaugh,E., Nott,A., Nwaokemeloh,O., Oregon,M., Ochi-Okorie,C., Odeh,E., Okwuonu,G., Okwuonu,K., Parker,D., Pasternak,S., Patel,B., Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T., Primus,E., Pu,L.-L., Puazo,M., Qin,X., Quinn,A., Quiroz,J., Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W., Santibanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y., Sisson,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Svatek,A., Taylor,E., Taylor,T., Thomas,N., Thorn,R., Thornton,R., Trejos,Z., Usmani,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D., Volkov,A., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J.,		

Wei, X., Wheeler, D., Williams, G., Williams, R., Worley, K., Wright, R.,
Wu, J., Yakub, S., Yan, K., Yuan, Y., Yu, F., Zhang, J., Zhang, L.,
Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 197215)

Worley, K.C.

Direct Submission

Submitted (04-SEP-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 197215)

REFERENCE

AUTHORS

CONSRPM

TITLE

JOURNAL

COMMENT

Bovine Genome Sequencing Consortium

Direct Submission

Submitted (23-JAN-2006) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jan 23, 2006 this sequence version replaced gi:74136772.

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with 'Ns' to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: FMSU

Center clone name: CH240-216G5

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 193754 bases at least Q40

Consensus quality: 194610 bases at least Q30

Consensus quality: 195146 bases at least Q20

Estimated insert size: 199308; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1637: contig of 1637 bp in length

* 1638 1687: gap of 50 bp

* 1688 22548: contig of 20861 bp in length

* 22549 23327: gap of 779 bp

* 23328 45680: contig of 22353 bp in length

* 45681 46082: gap of 402 bp

* 46083 168882: contig of 12800 bp in length

* 168883 168932: gap of 50 bp

* 168933 178836: contig of 9904 bp in length

* 178837 178886: gap of 50 bp

* 178887 194394: contig of 15508 bp in length

* 194395 194494: gap of unknown length

* 194495 195858: contig of 1364 bp in length

* 195859 195958: gap of unknown length

* 195959 197215: contig of 1257 bp in length.

* Location/Qualifiers

FEATURES

source

1. .197215
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-216G5"
1638. .1687
/estimated_length=50
22549. .23327
/estimated_length=779
45681. .46082
/estimated_length=402
168883. .168932
/estimated_length=50
178837. .178886
/estimated_length=50
194395. .194494
/estimated_length=unknown
195859. .195958
/estimated_length=unknown

ORIGIN

Query Match 24.0%; Score 168; DB 12; Length 197215;
Best Local Similarity 67.2%; Pred. No. 6.8e-39;
Matches 371; Conservative 0; Mismatches 120; Indels 61; Gaps 7;

Qy 173 TTTTAAATTTTAGTCACAGTTTTAGTCATTTCCTAATTTGAAAGTATCATAGTAATCC 232
Db 143403 TGTTCATATAAAGTTTTTTTTTAAATAATTTTCTAAGTAAAGCA--ATAAGTATCC 143346

Qy 233 ATAAATTTGAAAAAATGTTAACTACTCTGATATAAAAGTTTTATAGTTTCTCACTTTTA 292
Db 143345 ATGGAATTTGAAGGAGTGTAAATACTCTGATAAAGAGTTTCAGTTTTTC--TATTTC 143289

Qy 293 AGCAAAATTCATPAGGCGATGGTAATTTAGTTTCAACATTACTTGCAGTTTTCAGTTAGT 352
Db 143288 CACAAAAGTTTCGTTCTGCCTGTCTCATCTACAGTTTTAAACA-----TTCAGTTAGT 143240

Qy 353 AAATAAATTAAGCCTAGTAAGTATAATTTAATATTGTCAATAAATTTTGGAAAAATACCA 412
Db 143239 GAATGCATC-----TAAATTTAGTTTGTCTAAATAGCTAGGAATAATCA 143196

Qy 413 TGGGTACTTAATTTGATTTTACCAAAATTTCCATGGAACAAAACAAGTTTGGCTATTTTT-- 470
Db 143195 TGGGTATTTAATTTGGTTAAACTAAATTTCCACGGGAAAAATAGATAGGCTGGTTGTTT 143136

Qy 471 -----GGATTGATATTTTGAATACTAGTACAGGAATATCATTTGTTA 512
Db 143135 TGAGGGAGGGGAGAACAGGGATTGGTATTTTAAAAATACTAGTATAGGAGTGCATTTTA 143076

Qy 513 GTTGAATTTTTCAGCTTTAGAAAACAATGGAGTTTGTAGATAGCTAAAGTATAATTTATTG 572
Db 143075 G-----TTTTATCTTTTGAATAATTAATGCCGTTTAGTGAAGTATAATTTATTG 143021

Qy 573 TGATTTAATAATGGTATGGAGTTAGGCGTATGATAATTTAGTGAAAAACACCAAGAAATGTT 632
Db 143020 CAGTTTTCGAATGGTATGGTTTTTAATCTGCTGCTGTAATTTTGTGAAAAATACCATAGAGTTT 142961

Qy 633 TTATCTTTTAAATTT-----TTAAAAATTTGAATGACATTTGGAGTAAACATTCGCTTTTA 688
Db 142960 TTATGTTTTTAAATTTTAAATTTAAAGATTGGAATGACATTTTGGAAATGCAATTACCTTTTA 142901

Qy 689 GGTGATGTGGCA 700
Db 142900 GGTGATGTGGCA 142889

RESULT 3
AC074010/c
LOCUS
DEFINITION
Homo sapiens chromosome RPC1-11 clone RP11-707H2, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION
AC074010
VERSION
AC074010.4 GI:9858994

HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 159859)
 Waterston,R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 159859)
 Waterston,R.H.
 Direct Submission
 Submitted (09-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Aug 21, 2000 this sequence version replaced gi:9857594.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0707R02
 ----- Summary Statistics -----
 Sequencing vector: M13; 90%
 Sequencing vector: plasmid; 10%
 Chemistry: Dye-primer ET; 90% of reads
 Chemistry: Dye-terminator Big Dye; 10% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 154712 bases at least Q40
 Consensus quality: 156380 bases at least Q30
 Consensus quality: 157349 bases at least Q20
 Insert size: 150000; agarose-fp
 Insert size: 159259; sum-of-contigs
 Quality coverage: 6.07 in Q20 bases; agarose-fp
 Quality coverage: 5.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1
 * 5768: contig of 5768 bp in length
 * 5769
 * 5868: gap of unknown length
 * 5869
 * 16069: contig of 10201 bp in length
 * 16070
 * 16169: gap of unknown length
 * 16170
 * 32213: contig of 16044 bp in length
 * 32214
 * 32313: gap of unknown length
 * 32314
 * 50864: contig of 18551 bp in length
 * 50865
 * 50965: gap of unknown length
 * 50966
 * 74031: contig of 23067 bp in length
 * 74032
 * 74132: gap of unknown length
 * 74133
 * 106962: contig of 32831 bp in length
 * 106963
 * 107062: gap of unknown length
 * 107063
 * 159859: contig of 52797 bp in length.

Location/Qualifiers
 1. .159859
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="RP11-11"
 /clone="RP11-707H2"
 1. .5768
 /note="assembly_name:Contig8"
 5769. .5868
 /estimated_length=unknown
 5869. .16069
 /note="assembly_name:Contig9"
 16070. .16169

misc_feature
 gap
 misc_feature
 gap

 HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 159859)
 Waterston,R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 159859)
 Waterston,R.H.
 Direct Submission
 Submitted (09-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Aug 21, 2000 this sequence version replaced gi:9857594.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0707R02
 ----- Summary Statistics -----
 Sequencing vector: M13; 90%
 Sequencing vector: plasmid; 10%
 Chemistry: Dye-primer ET; 90% of reads
 Chemistry: Dye-terminator Big Dye; 10% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 154712 bases at least Q40
 Consensus quality: 156380 bases at least Q30
 Consensus quality: 157349 bases at least Q20
 Insert size: 150000; agarose-fp
 Insert size: 159259; sum-of-contigs
 Quality coverage: 6.07 in Q20 bases; agarose-fp
 Quality coverage: 5.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1
 * 5768: contig of 5768 bp in length
 * 5769
 * 5868: gap of unknown length
 * 5869
 * 16069: contig of 10201 bp in length
 * 16070
 * 16169: gap of unknown length
 * 16170
 * 32213: contig of 16044 bp in length
 * 32214
 * 32313: gap of unknown length
 * 32314
 * 50864: contig of 18551 bp in length
 * 50865
 * 50965: gap of unknown length
 * 50966
 * 74031: contig of 23067 bp in length
 * 74032
 * 74132: gap of unknown length
 * 74133
 * 106962: contig of 32831 bp in length
 * 106963
 * 107062: gap of unknown length
 * 107063
 * 159859: contig of 52797 bp in length.

Location/Qualifiers
 1. .159859
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="RP11-11"
 /clone="RP11-707H2"
 1. .5768
 /note="assembly_name:Contig8"
 5769. .5868
 /estimated_length=unknown
 5869. .16069
 /note="assembly_name:Contig9"
 16070. .16169

misc_feature
 gap
 misc_feature
 gap

repeat_region	/rpt_family="WIR"	17655..17812
repeat_region	/rpt_family=" (TAGA) n"	17881..18047
repeat_region	/rpt_family=" (TAGA) n"	18057..18542
repeat_region	/rpt_family="ERV1"	26846..26945
repeat_region	/rpt_family=" (TA) n"	26994..27171
repeat_region	/rpt_family=" (TA) n"	27209..27555
repeat_region	/rpt_family="ERV1"	27558..28081
repeat_region	/rpt_family="ERV1"	28585..29070
repeat_region	/rpt_family="MarR"	29120..29280
repeat_region	/rpt_family="L2"	29332..29516
repeat_region	/rpt_family="MER53"	

Query Match 16.5%; Score 115.6; DB 5; Length 172573;
Best Local Similarity 87.0%; Pred. No. 1.5e-23;
Matches 127; Conservative 0; Mismatches 19; Indels 0;

[illegible]

RESULT 5				
AC011079	AC011079	147859 bp	DNA	linear
LOCUS	Homo sapiens clone RP11-45I12,	WORKING DRAFT SEQUENCE, 4 unordered pieces.		
DEFINITION				
ACCESSION	AC011079			
VERSION	AC011079.3	GI:1136801		
KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAFT.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 147859)
Birtten,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-45112
Unpublished

2 (bases 1 to 147859)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Casle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Feireitz,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galgalian,J., Gardyna,S., Grant,G., Hagos,B., Headford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McDonald,L.J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

JOURNAL
TITLE
Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
Wyman, D., LeWitt, D., Zimmer, A. and Zogh, M.
Direct Submission

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 10, 2000 this sequence version replaced gi:7329251.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

```
----- Project Information
Center project name: L1162
Center clone name: 45112
```

Celler clone name: 43_1_12
----- Summary Statist

Sequencing vector: M13, M77815; 50% of reads
Sequencing vector: plasmid; n/a; 50% of reads
Chemistry: Dye-primer-aramsham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145316 bases at least Q40
Consensus quality: 146805 bases at least Q30
Consensus quality: 147173 bases at least Q20
Insert size: 142000; agarose-*fp*
Insert size: 147559; sum-of-*contigs*
Quality coverage: 11.4 in Q20 bases.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

Contig	Contig length (bp)	Contig	Contig length (bp)
28597	28597	28597	28597
28598	28598	28598	28598
28599	28599	28599	28599
28600	28600	28600	28600
28601	28601	28601	28601
28602	28602	28602	28602
28603	28603	28603	28603
28604	28604	28604	28604
28605	28605	28605	28605
28606	28606	28606	28606
28607	28607	28607	28607
28608	28608	28608	28608
28609	28609	28609	28609
28610	28610	28610	28610
28611	28611	28611	28611
28612	28612	28612	28612
28613	28613	28613	28613
28614	28614	28614	28614
28615	28615	28615	28615
28616	28616	28616	28616
28617	28617	28617	28617
28618	28618	28618	28618
28619	28619	28619	28619
28620	28620	28620	28620
28621	28621	28621	28621
28622	28622	28622	28622
28623	28623	28623	28623
28624	28624	28624	28624
28625	28625	28625	28625
28626	28626	28626	28626
28627	28627	28627	28627
28628	28628	28628	28628
28629	28629	28629	28629
28630	28630	28630	28630
28631	28631	28631	28631
28632	28632	28632	28632
28633	28633	28633	28633
28634	28634	28634	28634
28635	28635	28635	28635
28636	28636	28636	28636
28637	28637	28637	28637
28638	28638	28638	28638
28639	28639	28639	28639
28640	28640	28640	28640
28641	28641	28641	28641
28642	28642	28642	28642
28643	28643	28643	28643
28644	28644	28644	28644
28645	28645	28645	28645
28646	28646	28646	28646
28647	28647	28647	28647
28648	28648	28648	28648
28649	28649	28649	28649
28650	28650	28650	28650
28651	28651	28651	28651
28652	28652	28652	28652
28653	28653	28653	28653
28654	28654	28654	28654
28655	28655	28655	28655
28656	28656	28656	28656
28657	28657	28657	28657
28658	28658	28658	28658
28659	28659	28659	28659
28660	28660	28660	28660
28661	28661	28661	28661
28662	28662	28662	28662
28663	28663	28663	28663
28664	28664	28664	28664
28665	28665	28665	28665
28666	28666	28666	28666
28667	28667	28667	28667
28668	28668	28668	28668
28669	28669	28669	28669
28670	28670	28670	28670
28671	28671	28671	28671
28672	28672	28672	28672
28673	28673	28673	28673
28674	28674	28674	28674
28675	28675	28675	28675
2			

FEATURES

```

1. .147859
source
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-45112"
/clone_lib="RPCI-11 Human Male BAC"
misc_feature
1..28597
note="assembly_fragment"
clone_end:SP6
vector_side:left"
28598..28697
gap
estimated_length=100
28698..77950
misc_feature
note="assembly_fragment"
77951..78050
gap
estimated_length=100
78051..129172
misc_feature
note="assembly_fragment"
129173..129272
gap
estimated_length=100
129273..147859
misc_feature
note="assembly_fragment"
clone_end:T7
vector_side:right"

```

ORIGIN

```
Query Match      16.5%; Score 115.2; DB 12; Length 147859;
Best Local Similarity 87.5%; Pred. No. 2e-23;
Matches 126: Conservative 0; Mismatches 18; Indels 0; Gaps 0;
```

Qy

18 TTTT TTTT TTTT TGATGATT TTAATAAAATATCA TTTTC TTTTTTTT ATATTATAC TTTT 77

Db	89866	TTCATATTTTAAATTTTAAATAAAATTTATTTTATTTTATTTTAAATATATATATATACATTTT	89926
Qy	78	AACTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATATACATGTGCCCATG	137
Db	89926	AACTTTTAGGGTACATGAGCACAATATGCAGGTAGTTACATATGTATATATATGTGCCCATG	89985
Qy	138	CTGGTGTGCTGCACCACTAACTC	161
Db	89986	CTGGTATGCTGCACCACTATCTC	90009
RESULT 6			
LOCUS	AC025490	169821 bp	DNA linear HTG 28-MAR-2000
DEFINITION	Homo sapiens chromosome 4 clone RP11-6901 map 4, WORKING DRAFT SEQUENCE, 12 unordered pieces.		
ACCESSION	AC025490		
VERSION	AC025490.2	GI:73131510	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 169821)		
AUTHORS	Brirren,B., Linton,L., Nusbaum,C. and Lander,E.		
TITLE	Homo sapiens chromosome 4, clone RP11-6901		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 169821)		
AUTHORS	Brirren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campapiano,A., Castle,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,W., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehocsky,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Menues,L., Minova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tsafaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Mar 28, 2000 this sequence version replaced gi:7212073. All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html		
	----- Genome Center		
	Center: Whitehead Institute/ MIT Center for Genome Research		
	Center code: WIBR		
	Web site: http://www-seq.wi.mit.edu		
	Contact: sequence_submissions@genome.wi.mit.edu		
	----- Project Information		
	Center project name: L7352		
	Center clone name: 69 O.1		
	----- Summary Statistics		
	Chemistry vector: M13; M77815; 100% of reads		
	Assembly: Dye-terminator Big Dye; 100% of reads		
	Assembly program: Phrap; version 0.960731		
	Consensus quality: 163347 bases at least Q40		
	Consensus quality: 166674 bases at least Q30		
	Consensus quality: 167961 bases at least Q20		
	Insert size: 163000; agarose-ftp		

```
misc_feature /estimated_length=100
46960..65038
/note="assembly_fragment"
gap 65039..65138
/estimated_length=100
55139..84585
/note="assembly_fragment"
clone_end:T7
vector_side:right
84586..84685
/estimated_length=100
84686..111452
/note="assembly_fragment"
111453..111552
/estimated_length=100
111553..1136123
/note="assembly_fragment"
136124..136223
/estimated_length=100
136224..169821
/note="assembly_fragment"

ORIGIN
Query Match 16.5%; Score 115.2; DB 12; Length 169821;
Best Local Similarity 87.5%; Pred. No. 2e-23;
Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 18 TTTTTCATGATGTTTAAATAATATCATTTCTTTTATATATATATATATTTT 77
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
27858 TTCTATTTTAAATTTTAAATAATTTTATTTTATTTTAAATATATATATAT 27917
QY 78 AAGTTTGGGTACATGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTC 137
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
27918 AAGTTTGGGTACATGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTC 27977
QY 138 CTGGTGTGCTGCACCATTAATCTC 161
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
27978 CTGGTGTGCTGCACCATTAATCTC 28001

RESULT 7
AC093671/c 186370 bp DNA linear PRI 10-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-542P2 from 4, complete sequence.
ACCESSION AC093671
VERSION AC093671.3 GI:17861069
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 186370)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 186370)
AUTHORS Holmes,A., Elliott,G. and Kozlowski,A.
TITLE The sequence of Homo sapiens BAC clone RP11-542P2
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 186370)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 186370)
Waterston,R.H.
Direct Submission
JOURNAL Submitted (15-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
```

```
REFERENCE 5 (bases 1 to 186370)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 186370)
Waterston,R.
Direct Submission
JOURNAL Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 15, 2001 this sequence version replaced gi:16259163.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
-----
Center project name: H_NH0542P02
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC048378; the clone sequenced to
the right is RP11-5K16. Actual start of this clone is at base
position 1 of RP11-542P2; actual end is at base position 186370 of
RP11-542P2.

Data from AC048378, AC025490 and AC010954 was used to finish the
clone, AC093671. Single plasmid region exists between 150675 and
150731.

FEATURES
source
1. 186370
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-542P2"
/clone_lib="RPCI-11"
1..24
misc_feature
/note="match to EST BM021296 (NID:gl6535652) ie75d01.y1"
4..295
repeat_region
/rpt_family="Alu"
4..22
misc_feature
```


Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160248 bases at least Q40
Consensus quality: 160506 bases at least Q30

Consensus quality: 160675 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 160743; sum-of-contigs
Quality coverage: 10.74x in Q20 bases; agarose-fp
Quality coverage: 11.89x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 25268: contig of 25268 bp in length
25269 25368: gap of unknown length
25369 40449: contig of 15081 bp in length
40450 40549: gap of unknown length
40550 47926: contig of 7377 bp in length
47927 48026: gap of unknown length
48027 55497: contig of 7471 bp in length
55498 55597: gap of unknown length
55598 92427: contig of 36830 bp in length
92428 92527: gap of unknown length
92528 96210: contig of 3683 bp in length
96211 96310: gap of unknown length
96311 161343: contig of 65033 bp in length.

FEATURES

source	Location/Qualifiers
1. .161343	/organism="Pan troglodytes"
	/mol_type="genomic DNA"
	/db_xref="taxon:9598"
	/clone="CH251-287A2"
	/clone_lib="CH251"
misc_feature	1. .85615
	/note="clone overlaps with GenBank Accession Number AC099408 clone RP43-44D23 (center project name cmb)"
misc_feature	1. .25268
	/note="assembly_fragment clone_end:T7 vector_side:left"
gap	25269..25368
	/estimated_length=unknown
misc_feature	25369..40449
	/note="assembly_fragment"
gap	40450..40549
	/estimated_length=unknown
misc_feature	40550..47926
	/note="assembly_fragment"
gap	47927..48026
	/estimated_length=unknown
misc_feature	48027..55497
	/note="assembly_fragment"
gap	55498..55597
	/estimated_length=unknown
misc_feature	55598..92427
	/note="assembly_fragment"
gap	92428..92527
	/estimated_length=unknown
misc_feature	92528..96210
	/note="assembly_fragment"
gap	96211..96310
	/estimated_length=unknown
misc_feature	96311..161343
	/note="assembly_fragment clone_end:SP6 vector_side:right"

ORIGIN

Query Match 16.3%; Score 114.4; DB 12; Length 161343;
Best Local Similarity 83.3%; Pred. No. 3.4e-23;
Matches 130; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	6	TCACATAAAGCTTTTTCATGATTTTAAATAATATCATTTCTTTTATTAT 65
Db	77227	TAAATTACAATGGTTTTTTCATGATTAACAGTAACATTTTATTATTAT 77286
QY	66	TATTATACCTTTTAAAGTTTTCATGATTTTAAATAATATCATTTCTTTTATTAT 125
Db	77287	TATTATACCTTTTAAAGTTTTCATGATTTTAAATAATATCATTTCTTTTATTAT 77346
QY	126	ACATGTGCCATGCTGTGTGCTGCACCACTTAATC 161
Db	77347	ACATGTGCCATGCTGTGTGCTGCACCACTTAATC 77382

RESULT 10

AC021134	LOCUS	Homo sapiens BAC clone RP11-402D23 from 4, complete sequence.	DNA	linear	PRI 09-JAN-2002
AC021134	DEFINITION	Homo sapiens BAC clone RP11-402D23 from 4, complete sequence.			
AC021134	ACCESSION				
AC021134.8	VERSION	GI:14702086			
HTG.	KEYWORDS				
Homo sapiens (human)	SOURCE				
Homo sapiens	ORGANISM				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
Hominidae; Homo.					
1 (bases 1 to 135692)	REFERENCE				
Sulston,J.E. and Waterston,R.	AUTHORS				
Toward a complete human genome sequence	TITLE				
Genome Res. 8 (11), 1097-1108 (1998)	JOURNAL				
9847074	PUBMED				
2 (bases 1 to 135692)	REFERENCE				
Haglund,K., Kozlowski,A., Hawkins,M. and Spalding,L.	AUTHORS				
The sequence of Homo sapiens BAC clone RP11-402D23	TITLE				
Unpublished (2001)	JOURNAL				
3 (bases 1 to 135692)	REFERENCE				
Waterston,R.H.	AUTHORS				
Direct Submission	TITLE				
Submitted (14-JAN-2000) Genome Sequencing Center, Washington	JOURNAL				
University School of Medicine, 4444 Forest Park Parkway, St. Louis,					
MO 63108, USA					
4 (bases 1 to 135692)	REFERENCE				
Waterston,R.H.	AUTHORS				
Direct Submission	TITLE				
Submitted (12-JUL-2001) Genome Sequencing Center, Washington	JOURNAL				
University School of Medicine, 4444 Forest Park Parkway, St. Louis,					
MO 63108, USA					
5 (bases 1 to 135692)	REFERENCE				
Waterston,R.	AUTHORS				
Direct Submission	TITLE				
Submitted (09-JAN-2002) Department of Genetics, Washington	JOURNAL				
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA					
On Jul 12, 2001 this sequence version replaced gi:14573744.	COMMENT				
----- Genome Center					
Center: Washington University Genome Sequencing Center					
Center code: WUGSC					
Web site: http://genome.wustl.edu/gsc					
Contact: sapiens@wustl.wustl.edu					
----- Summary Statistics					

Center project name: H_NH0402D23					

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC005150, 2000 bp overlap. Actual end of this clone is at base position 135692 of RP11-402D23.

Polymorphisms have been identified between AC005150 and RP11-402D23.

FEATURES

source

Location/Qualifiers

1..135692
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"

/clone="RP11-402D23"
/clone_lib="RPCI-11"

1..91
/rpt_family="ERV1"

92..532
/rpt_family="ERV1"

571..686
/rpt_family="MIR"

1337..1395
/rpt_family="GA-rich"

2219..2247
/rpt_family="(T)n"

4589..4646
/rpt_family="(ATG)n"

4963..5271
/rpt_family="L1"

5744..5815
/rpt_family="AT-rich"

6349..6382
/rpt_family="(TA)n"

6437..6628
/rpt_family="(TA)n"

6982..7229
/rpt_family="L1"

7208..7255
/rpt_family="A-rich"

8877..9023
/rpt_family="ERV1"

9493..9757
/rpt_family="MIR"

10395..10424
/rpt_family="AT-rich"

10818..10927
/rpt_family="MER1_type"

11356..11482
/rpt_family="Alu"

11476..11541
/rpt_family="(TA)n"

11545..11707
/rpt_family="Alu"

12184..12212
/rpt_family="(A)n"

repeat_region 15073..15665
/rpt_family="ERV1"
repeat_region 15708..16234
/rpt_family="ERV1"
repeat_region 16344..16645
/rpt_family="L2"
repeat_region 17208..17256
/rpt_family="(TATG)n"
repeat_region 21435..21631
/rpt_family="MIR"
repeat_region 21610..21637
/rpt_family="AT-rich"
repeat_region 21750..21820
/rpt_family="GA-rich"
repeat_region 21864..22532
/rpt_family="ERV1"
repeat_region 23064..23092
/rpt_family="AT-rich"
repeat_region 23253..23547
/rpt_family="Alu"
repeat_region 23552..23596
/rpt_family="(GGAA)n"
repeat_region 23636..23835
/rpt_family="L1"
repeat_region 24614..24707
/rpt_family="L2"
repeat_region 25286..25758
/rpt_family="ERV1"
repeat_region 25814..26866
/rpt_family="ERV1"
repeat_region 26291..26313
/rpt_family="AT-rich"
repeat_region 27735..28061
/rpt_family="Alu"
repeat_region 27861..27884
/rpt_family="(A)n"
repeat_region 28036..28062
/rpt_family="(GAA)n"
repeat_region 28108..28660
/rpt_family="ERV1"
repeat_region 28898..29396
/rpt_family="ERV1"
repeat_region 29857..30047
/rpt_family="MIR"
repeat_region 30674..30965
/rpt_family="L2"
repeat_region 31191..31434
/rpt_family="MIR"
repeat_region 32080..32373
/rpt_family="L2"
repeat_region 32660..32718
/rpt_family="MER1_type"
repeat_region 33053..33255
/rpt_family="MIR"
repeat_region 34203..34248
/rpt_family="CR1"
repeat_region 36190..36663
/rpt_family="L1"
repeat_region 36826..36956
/rpt_family="L1"
repeat_region 37137..37158
/rpt_family="AT-rich"
repeat_region 37165..37464
/rpt_family="Alu"
repeat_region 37447..37472
/rpt_family="AT-rich"
repeat_region 37474..38152
/rpt_family="L1"
repeat_region 38145..38167
/rpt_family="AT-rich"

Query Match

Best Local Similarity 16.3%; Score 114; DB 5; Length 135692;
86.7%; Pred. No. 4.6e-23;

GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:41:39 ; Search time 517 Seconds
(without alignments)
940.182 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_A146311

Perfect score: 700

Sequence: 1 ctgtttcacataaagttttt.....gccttttagtgatgtgga 700

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

N_Geneseq 8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	699.6	100.0	190276	14	ADY94258	ADY94258 BRAF prot
C 2	113.2	16.2	19167	4	AA105340	AA105340 Human rep
C 3	113.2	16.2	19167	4	AB198209	AB198209 Human tes
4	113.2	16.2	19167	5	ABR19101	ABR19101 Human ner
5	113.2	16.2	155225	12	ADQ59197	ADQ59197 MSI-H car
6	106.8	15.3	8766	12	ADJ12500	ADJ12500 DNA fragm
7	106.6	15.2	8666	4	AA546305	AA546305 Tumour su
8	106.6	15.2	8666	6	ABL32396	ABL32396 Human imm
9	106.6	15.2	8666	6	ABK34008	ABK34008 Human DNA
10	106.6	15.2	8666	6	ABQ67177	ABQ67177 Human ang
11	106.6	15.2	8666	10	ADB54111	ADB54111 Pretreate
12	106.6	15.2	8666	10	ADB54239	ADB54239 Pretreate
13	106.6	15.2	8666	10	ADE84177	ADE84177 Human lym
14	106.6	15.2	8666	10	ADE84101	ADE84101 Human lym
15	106.6	15.2	8666	13	ADS89541	ADS89541 Oligonuc
16	106.6	15.2	8666	13	ADS89267	ADS89267 Oligonuc
17	105.6	15.1	70043	12	ADO48201	ADO48201 Human p21
C 18	105.4	15.1	82938	6	ABV72623	ABV72623 Human tra

19	105	15.0	110000	14	AD245062	06	Continuation (7 of
20	104.6	14.9	72678	13	ABD33207		Abd33207 Human can
C 21	104.2	14.9	42595	12	ADJ12615		Adj12615 DNA fragm
C 22	104	14.9	127369	11	ACN44006		Acn44006 Human gen
C 23	104	14.9	191150	12	ADM69029		Adm69029 Human pla
C 24	103.8	14.8	87472	14	AD213131		Ad213131 Human can
C 25	103.8	14.8	102980	11	ACN44734		Acn44734 Human gen
C 26	103.6	14.8	110000	6	ABL57909	1	Continuation (2 of
C 27	103.6	14.8	110300	13	ADS36499		Ads36499 Human aut
C 28	103.4	14.8	3200	5	AA576297		AA576297 DNA encod
C 29	103.4	14.8	70665	6	ABT10716		Abt10716 Human bre
C 30	103.4	14.8	70665	11	ADN95672		Adn95672 Human BEC
C 31	103.2	14.7	24132	4	AAK68729		Aak68729 Human 1mm
C 32	103.2	14.7	24132	4	AA528227		Aas28227 Genomic s
C 33	103.2	14.7	24132	10	ADG41423		Adg41423 Human res
C 34	103.2	14.7	24132	11	ADI97197		Adi97197 Human res
C 35	103.2	14.7	118544	12	ADQ97100		Adq97100 Human can
C 36	102.8	14.7	277616	13	ABD32602		Abd32602 Human can
C 37	102.6	14.7	26225	4	AA535776		Aas35776 Human car
C 38	102.6	14.7	26225	10	ADE46470		Ade46470 Human car
C 39	102.6	14.7	26225	12	ADJ12594		Adj12594 DNA fragm
C 40	102.6	14.7	26225	13	ADJ07888		Adj07888 Human car
C 41	102.6	14.7	56423	10	ADC85728		Adc85728 Human GPC
C 42	102.6	14.7	144460	3	AA293815		Aaz293815 Olfactory
C 43	102.4	14.6	21597	12	ADJ12455		Adj12455 DNA fragm
C 44	102.2	14.6	390	9	ACH16304		Ach16304 Human adu
C 45	102.2	14.6	734	11	ACN91262		Acn91262 Breast ca
C 46	101.8	14.5	344548	11	ACN44070		Acn44070 Human gen
C 47	101.4	14.5	325	3	AA14867		Aac14867 Human sec
C 48	101.4	14.5	35357	6	ABN85746		Abn85746 Human tra
C 49	101.4	14.5	326014	6	ABK89296		Abk89296 Human gen
C 50	101.4	14.5	326014	12	ADQ94981		Adq94981 Human kin
C 51	101.2	14.5	96594	10	ADE95974		Ade95974 Human SYK
C 52	101.2	14.5	96595	9	ADA02726		Ada02726 Human SYK
C 53	101.2	14.5	96595	10	ADB72464		Adb72464 Human SYK
C 54	101.2	14.5	334462	10	ADC24763		Adc24763 Human wil
C 55	101	14.4	76329	15	AEF22520		Aef22520 Double co
C 56	100.8	14.4	183337	8	ABQ77402		Abq77402 Human EDN
C 57	100.8	14.4	238484	11	ACN44210		Acn44210 Human gen
C 58	100.4	14.3	1055	12	ADJ12600		Adj12600 DNA fragm
C 59	100.4	14.3	1055	12	ADJ12572		Adj12572 DNA fragm
C 60	100.4	14.3	181257	12	ADF69677		Adf69677 Human SLC
C 61	100.4	14.3	326014	6	ABK89296		Abk89296 Human gen
C 62	100.4	14.3	326014	12	ADQ94981		Adq94981 Human kin
C 63	100	14.3	91359	13	ABD32673		Abd32673 Human can
C 64	100	14.3	178863	15	AEF74795		Aef74795 Human pol
C 65	99.8	14.3	607	4	AAK91185		Aak91185 Human dig
C 66	99.8	14.3	607	5	AA532117		Aas32117 Human liv
C 67	99.8	14.3	607	6	ABN90472		Abn90472 Human liv
C 68	99.8	14.3	607	11	ADJ15385		Adj15385 Human liv
C 69	99.8	14.3	8666	10	ADB53962		Adb53962 CDKN2a ge
C 70	99.8	14.3	8666	10	ADE84023		Ade84023 5' regula

ALIGNMENTS

RESULT 1

ADY94258

ID ADY94258 standard; DNA; 190276 BP.

XX ADY94258;

AC ADY94258;

DT 16-JUN-2005 (first entry)

XX BRAF protein kinase gene DNA sequence.

DE BRAF protein kinase; melanoma; cytostatic; diagnosis; DNA polymorphism;

XX drug screening; chromosome-7q34; gene therapy; BRAF; ds; gene;

KW single nucleotide polymorphism; SNP.

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers
FT variation 64547
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT variation 68398
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT variation 76779
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT variation 80400
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT variation 87826
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT variation 98682
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT variation 98946
FT /*tag= g
FT /standard_name= "Single nucleotide polymorphism"
FT variation 118712
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphism"
FT variation 128002
FT /*tag= i
FT /standard_name= "Single nucleotide polymorphism"
FT variation 132526
FT /*tag= j
FT /standard_name= "Single nucleotide polymorphism"
FT variation 138875
FT /*tag= k
FT /standard_name= "Single nucleotide polymorphism"
FT variation 146311
FT /*tag= l
FT /standard_name= "Single nucleotide polymorphism"
XX WO2005027710-A2.
XX 31-MAR-2005.
XX 11-SEP-2003; 2003WO-US028788.
XX 11-SEP-2002; 2002US-0410595P.
XX 29-OCT-2002; 2002US-0422344P.
XX (SEQU-) SEQUENOM INC.
XX Roth RB, Nelson MR, Braun A;
XX WPI; 2005-273028/28.
XX Identifying a subject at risk of melanoma, useful for treating or
XX preventing melanoma by detecting the presence or absence of one or more
XX polymorphic variations associated with melanoma in a nucleic acid sample
XX from a subject.
XX Claim 1; SEQ ID NO 1; 175pp; English.
XX The new invention relates to the discovery that polymorphic variations in
XX a gene (ADY94258) encoding a BRAF protein kinase is associated with the
XX occurrence of melanoma. BRAF is a serine/threonine protein kinase and is
XX a member of the RAF family. It participates in the RAS/RAF/MEK/ERK/MAP
XX kinase signal transduction pathway. The BRAF gene is located on
XX chromosome 7q34 (assembly 30). Provided are methods of identifying a
XX subject at risk of melanoma by detecting the presence or absence of one
XX or more polymorphic variations in BRAF associated with melanoma in a
XX nucleic acid sample from a subject. Also disclosed is a method of
XX identifying a polymorphic variation associated with melanoma proximal to
XX an incident polymorphic variation associated with melanoma. Also
XX disclosed is a method of identifying a candidate molecule that modulates
XX cell proliferation by introducing a test molecule to a system which

CC comprises the nucleic acid; and determining the presence or absence of an
CC interaction between the test molecule and the nucleic acid or protein.
CC The polymorphic variations are detected at one or more positions in
CC ADY94258. The positions are in linkage disequilibrium with one or more
CC positions in SEQ ID No. 1, or the variation is the haplotype CTGG or ATGA
CC in ADY94258. Detecting the presence or absence of the one or more
CC polymorphic variations comprises hybridizing an oligonucleotide to the
CC nucleic acid sample, where the oligonucleotide hybridizes to a region
CC adjacent to the polymorphic variation. The proximal polymorphic variation
CC is within a region between about 5 kb 5' of the incident polymorphic
CC variation and about 5 kb 3' of the incident polymorphic variation.
CC Treating melanoma in a subject alternatively comprises contacting one or
CC more cells of a subject with a duplex RNA nucleic acid. The invention is
CC useful for treating or preventing melanoma. The present sequence is the
CC DNA sequence of the human BRAF gene.
XX
SQ Sequence 190276 BP; 55599 A; 35097 C; 37143 G; 62425 T; 0 U; 12 Other;
Query Match 100.0%; Score 700; DB 14; Length 190276;
Best Local Similarity 99.9%; Pred. No. 5e-110; Indels 0; Gaps 0;
Matches 699; Conservative 1; Mismatches 0;
Qy 1 CTGTTTCACATAAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTTT 60
Db CTGTTTCACATAAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTTT 146060
Qy 61 ATTATATTATATCTTTTAAGTTTATAGGTACATGTGCAAGTGTGCAGTTAGTACATA 120
Db ATTATATTATATCTTTTAAGTTTATAGGTACATGTGCAAGTGTGCAGTTAGTACATA 146120
Qy 121 TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACCTACATCAAGTTTTTTTTTAAA 180
Db TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACCTACATCAAGTTTTTTTTTAAA 146180
Qy 181 TTTTAGTGACAGTTTATAGTCATTTTCTTAATTTGAAAGTATCATAGTAATCCATAAATTT 240
Db TTTTAGTGACAGTTTATAGTCATTTTCTTAATTTGAAAGTATCATAGTAATCCATAAATTT 146240
Qy 241 GAAAAAATGTTAACTACTCTGTATAAAAAAGTTTTTATAGTTTCTTACTTTTAAAGCAAAAT 300
Db GAAAAAATGTTAACTACTCTGTATAAAAAAGTTTTTATAGTTTCTTACTTTTAAAGCAAAAT 146300
Qy 301 TCCATAGGGCATGCTAATTTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATAAAT 360
Db TCCATAGGGCATGCTAATTTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATAAAT 146360
Qy 361 ATTAAGCCTAGTAAGTATTAATTTAATTTATTTGTCATAAATTTGGAAAAATACCCTGGGTACT 420
Db ATTAAGCCTAGTAAGTATTAATTTAATTTATTTGTCATAAATTTGGAAAAATACCCTGGGTACT 146420
Qy 421 TAATTGATTTTACCAAAATTTCCATGGAACAAACAAAGTTGGCTATTTTGGATTGTATAT 480
Db TAATTGATTTTACCAAAATTTCCATGGAACAAACAAAGTTGGCTATTTTGGATTGTATAT 146480
Qy 481 TTTGAAATACTAGTACAGGAATATCATTTGTAGTTGAAATTTTAGCCTTAGAAAAACAAT 540
Db TTTGAAATACTAGTACAGGAATATCATTTGTAGTTGAAATTTTAGCCTTAGAAAAACAAT 146540
Qy 541 GGAGTTTAGATAGTAAAGTATTAATTTATTTGATTTTAAATAATGGTATGGAGTTAGGCG 600
Db GGAGTTTAGATAGTAAAGTATTAATTTATTTGTGATTTTAAATAATGGTATGGAGTTAGGCG 146600
Qy 601 TATGATAAATAGTGAACAAACACCAAGATGTTTTTATATCTTTTAAATTTTAAATAATTCAAA 660
Db TATGATAAATAGTGAACAAACACCAAGATGTTTTTATATCTTTTAAATTTTAAATAATTCAAA 146660
Qy 661 TGACACTTGGAGTAACAAATTCCTTTTAGGTGATGGCA 700
Db TGACACTTGGAGTAACAAATTCCTTTTAGGTGATGGCA 146700

AAAL05340 standard; DNA; 19167 BP.
AAAL05340;
21-NOV-2001 (first entry)
Human reproductive system related antigen DNA SEQ ID NO: 8028.
Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy; ds.
Homo sapiens.
WO200155320-A2.
02-AUG-2001.
17-JAN-2001; 2001WO-US001339.
31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0209467P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225213P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225267P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225759P.
22-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226868P.
22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-0229287P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0232080P.
08-SEP-2000; 2000US-0232081P.
12-SEP-2000; 2000US-0231968P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233065P.
21-SEP-2000; 2000US-0234223P.
21-SEP-2000; 2000US-0234274P.
25-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-0234998P.
26-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241836P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
01-DEC-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
05-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.

```
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
XX Disclosure; SEQ ID NO 8028; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
XX Sequence 19167 BP; 5824 A; 3876 C; 3875 G; 5592 T; 0 U; 0 Other;
SQ
Query Match 16.2%; Score 113.2; DB 4; Length 19167;
Best Local Similarity 82.3%; Pred. No. 2.1e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 4 TTTCACATAAGTTTTTTTTTTTGATGATTTTAATAAAATATCATTTCTTTTTTTTATT 63
Db 10109 TTATACTAACTTTTTTTTTTTTGGCTTGGAAATCTTTTTTTTTTAATTATT 10050
Qy 64 ATTATTATACTTTAAAGTTTATAGGTCATGTCGAAAGTGGCAGGTAGTTACATATAT 123
Db 10049 ATTATTATACTTTAAAGTTTATAGGTCATGTCGAAAGTGGCAGGTAGTTACATAT 9990
Qy 124 ATACATGTCGATGCTGGTGTGCTGACCCATTAACTC 161
Db 9989 ATACATGTCGATGCTGGTGTGCTGACCCATTAACTC 9952
RESULT 3
ABL98209/c
ID ABL98209 standard; DNA; 19167 BP.
XX
AC ABL98209;
XX
XX 21-JUN-2002 (first entry)
XX
XX Human testicular antigen encoding DNA fragment SEQ ID NO: 2861.
DE
XX
XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX WO20015317-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001329.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232403P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 25-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
```


PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 14-AUG-2000; 2000US-0226275P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227099P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 06-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 01-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system cancers
XX and metastases.
XX
XX Disclosure; SEQ ID NO 11432; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
XX (AB14678-AB18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischaemia; (d) wound healing
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infectious diseases such as viral, bacterial, fungal and parasitic
XX infections. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 19167 BP; 5592 A; 3875 C; 3876 G; 5824 T; 0 U; 0 Other;
SQ

Query Match 16.2%; Score 113.2; DB 5; Length 19167;
Best Local Similarity 82.3%; Pred. No. 2.1e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 TTTCCATATAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTCTTTTTTTTATT 63
DB 9059 TTATAACTAACTTTTTTTTTTTTGGCTTGGAAATCTTTTTTTTTTTAAATTTATT 9118

QY 64 ATTATTATACTTTAAAGTTTTTAGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 123
DB 9119 ATTATTATACTTTAAAGTTTTTAGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 9178

QY 124 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 161
DB 9179 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 9216

RESULT 5
ADQ59197
ID ADQ59197 standard; DNA; 155225 BP.
XX
AC ADQ59197;
XX
DT 09-SEP-2004 (first entry)
XX
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.
XX
KW coding mononucleotide repeat; CMNR; gene; antibody; MSI-H tumour;
KW MSI-H carcinoma; high microsatellite instability tumour;
KW high microsatellite instability carcinoma; cytostatic; ds.

OS Homo sapiens.
XX
FN KR2004008012-A.
XX
PD 28-JAN-2004.
XX
PF 15-JUL-2002; 2002KR-00041304.
XX
PR 15-JUL-2002; 2002KR-00041304.
XX
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
XX
PI Kim HG, Kim NG, Lee JS, Rhee HS;
XX
WPI; 2004-386326/36.

Genes containing coding mononucleotide repeats are useful in developing an antibody against MSI-H (hugh (sic high) microsatellite instability) tumor.

Claim 3; SEQ ID NO 34; 578pp; Korean.

The present invention describes genes containing coding mononucleotide repeats (CMNRs). The genes are useful for the development of an antibody against MSI-H (hugh microsatellite instability) tumour. Also described: (1) cDNA genes containing CMNRs with 10 or more nucleotide sequences, and selected from the cDNA genes having the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 and 43; (2) cDNA genes, which are frameshift mutated by deletion or insertion of one or more base in the CMNRs; (3) genomic DNA genes containing CMNRs with 10 or more nucleotide sequences, and selected from the genomic DNA genes having the nucleotide sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift mutated by deletion or insertion of one or more base in the CMNRs. The genes have cytostatic activity. The present sequence represents an MSI-H carcinoma genomic DNA sequence from the present invention.

XX

SQ Sequence 155225 BP; 44334 A; 29321 C; 30431 G; 51139 T; 0 U; 0 Other;
Query Match 16.2%; Score 113.2; DB 12; Length 155225;
Best Local Similarity 82.3%; Pred. No. 2e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 TTTCCATATAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTCTTTTTTTTATT 63
DB 138460 TTATAACTAACTTTTTTTTTTTTGGCTTGGAAATCTTTTTTTTTTTAAATTTATT 138519

QY 64 ATTATTATACTTTAAAGTTTTTAGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 123
DB 138520 ATTATTATACTTTAAAGTTTTTAGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 138579

QY 124 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 161
DB 138580 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 138617

RESULT 6
ADJ12500
ID ADJ12500 standard; DNA; 8766 BP.
XX
AC ADJ12500;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq354.
XX
KW human; secreted; cancer; haematopoietic disease; anaemia;
KW multiple myeloma; reproductive system disorder; prostatitis;
KW inguinal hernia; musculoskeletal disease; systemic lupus erythematosus;
KW gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
KW fetal alcohol syndrome; Down's syndrome; excretory disease;
KW urinary incontinence; renal disorder; neural; sensory disease;
KW Alzheimer's disease; meningitis; respiratory disease; emphysema;
KW occupational lung disease; endocrine disease; diabetes;
KW glomerulonephritis; digestive disease; portal hypertension;
KW irritable bowel syndrome; epithelial disease; scleroderma;
KW epidermolysis bullosa; cytostatic; antineoplastic; antiarthritic;
KW antipsoriatic; anti-HIV; immunosuppressive; antiinflammatory;
KW antiparasitic; antibacterial; osteopathic; dermatological; antigout;
KW immunomodulator; antiarrhythmic; cardiac; nootropic; antileptic;
KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
KW antidiabetic; anabolic; hypertensive; vulnery; ds.

OS Homo sapiens.

XX
XX
XX US2004010132-A1.

XX
XX
XX 15-JAN-2004.

XX
XX
XX 30-OCT-2001; 2001US-00984429.

XX
XX
XX 09-OCT-1997; 97US-0061463P.

XX
XX
XX 09-OCT-1997; 97US-0061527P.

XX
XX
XX 09-OCT-1997; 97US-0061529P.

XX
XX
XX 09-OCT-1997; 97US-0061532P.

XX
XX
XX 09-OCT-1997; 97US-0061536P.

XX
XX
XX 09-OCT-1997; 97US-0071498P.

XX
XX
XX 08-OCT-1998; 98WO-US021142.

XX
XX
XX 08-APR-1999; 99US-00288143.

XX
XX
XX 01-NOV-2000; 2000US-0244591P.

XX
XX
XX (ROSE/) ROSEN C A.

XX
XX
XX (BREW/) BREWER L A.

XX
XX
XX (DUAN/) DUAN R D.

XX
XX
XX (RUBE/) RUBEN S M.

XX
XX
XX (FLOR/) FLORENCE K A.

XX
XX
XX (GREE/) GREENE J M.

XX
XX
XX (YOUN/) YOUNG P E.

XX
XX
XX (FERR/) FERRIE A M.

XX
XX
XX (YUGG/) YU G.

PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
XX
PI Rosen CA, Brewer LA, Duan RD, Ruben SM, Florence KA, Greene JM;
PI Young PE, Ferrie AM, Yu G, Florence C, Ebner R, Olsen H;
XX WPI; 2004-090518/09.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating, preventing or ameliorating diseases or disorders e.g. cancer,
PT anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
PT disease.
XX
PS Disclosure; SEQ ID NO 354; 286pp; English.
XX
XX This invention relates to novel polynucleotides encoding human secreted
CC proteins. Specifically, it refers to the vectors, host cells, recombinant
CC and synthetic methods for producing human polynucleotides, polypeptides
CC and antibodies. Furthermore, it relates to screening methods to identify
CC agonists and antagonists that can be used to inhibit or enhance the
CC production and function of the secreted proteins. The present invention
CC describes these compositions as useful for diagnosing, treating or
CC preventing disorders such as cancer, haematopoietic diseases including
CC anaemia and multiple myeloma, reproductive system disorders including
CC prostatitis and inguinal hernia, musculoskeletal diseases including
CC systemic lupus erythematosus and gout, cardiovascular disease including
CC arrhythmia and hypernatraemia, mixed fetal diseases including fetal
CC alcohol syndrome and Down's syndrome, excretory diseases including
CC urinary incontinence and renal disorders, neural or sensory disease
CC including Alzheimer's disease and meningitis, respiratory disease
CC including emphysema and occupational lung disease, endocrine diseases
CC including diabetes and glomerulonephritis, digestive diseases including
CC portal hypertension and irritable bowel syndrome and connective tissue or
CC epithelial diseases including scleroderma and epidermolysis bullosa. As
CC such, there are various activities such as cytostatic, antianemic,
CC antiarthritic, antiasthmatic, anti-HIV, immunosuppressive,
CC antiinflammatory, antipsoriatic, antibacterial, osteopathic,
CC dermatological, antigout, immunomodulator, antiarrhythmic, cardiant,
CC neurotropic, antilipemic, nephrotropic, uropathic, neuroprotective,
CC antiparkinsonian, tranquilizer, antidiabetic, anabolic, hypertensive and
CC vulnerary. This polynucleotide is a DNA fragment of a BAC clone that
CC encodes a human secreted protein of the invention. NOTE: This sequence
CC does not appear in the printed specification but has been obtained in
CC electronic format from the US patent office at the following web site
CC www.seqdata.uspto.gov/sequence.html; Document ID: 20040010132.
XX
SQ Sequence 8766 BP; 2308 A; 1479 C; 1597 G; 3382 T; 0 U; 0 Other;
Query Match 15.3%; Score 106.8; DB 12; Length 8766;
Best Local Similarity 94.1%; Pred. No. 2.6e-09;
Matches 111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 44 TATCATTTCTTTTTTTTATTATTATTATCTTTTAAAGTTTAGGGTACATGTCGCAAGTG 103
DB 2 TTTTATTTTATTTTATTATTATTATTATATCTTTTAAAGTTTAGGGTACATGTCGCAATG 61
QY 104 TGCAGGTTAGTACATATATATACATGTCGCTGGTGGTGGTGCACCACTAACTC 161
DB 62 TGCAGGTTAGTACATATATATACATGTCGCTGGTGGTGGTGCACCACTAACTC 119
RESULT 7
AAS46305
ID AAS46305 standard; DNA; 8666 BP.
XX
AC AAS46305;
XX
DT 18-DEC-2001 (first entry)
XX
XX Tumour suppressor gene derived chemically modified sequence #27.
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW

KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
XX Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-EP002955.
XX
XX 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-602752/68.
XX
XX Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
XX Claim 1; SEQ ID NO 27; 27pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
Query Match 15.2%; Score 106.6; DB 4; Length 8666;
Best Local Similarity 49.0%; Pred. No. 2.9e-09;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;
QY 12 AAAGTTTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTATTATTAT 71
DB 1547 AAAGTTTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTATTATTAT 1606
QY 72 ACTTTTAAAGTTTTTAGGGTACATGTCGCAAGTGGCAGGTAGTTACATATATATACATGT 131
DB 1607 TATTTTAAAGTTTTTAGAGTATATGTTGTAATGTTAGTTTGTATATATATATATGT 1666
QY 132 GCCATGCTGGTGGTGCACCCCACTAACTCACAATGAAGTTTTTTTTTAAATTTTAGTGACA 191
DB 1667 GTTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1725
QY 192 GTTTTAGTCATTTTTCCTTAATTTGAAAGTATCATAGTAATCCATAAATTTTGAAGAAATGT 251
DB 1726 GTTATTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1785

Qy	252	TAAC	TACTCTCGATAAAAAGTTTATAGTTTCCTACTCTTTTAAGCAAAATCCCATAGGCCA	311
Db	1786	AGAG	TAAATGGTTTATTTTAAAGATGTTATAATTTTTTTAGAGTTTATTTGTAAGATAT	1845
Qy	312	TGGT	AAATTGTAGTTTCAACATTACTGTCAGTTTCAGTTAGTAAATAATATTAAAGCCTAG	371
Db	1846	GAGT	ATATATATTTTAAAAATTTGGTTATTTTTTAAAGTAGTTAAATTTTTTATATTG	1905
Qy	372	TAAG	TATATAATTTAAATATTGTGCAAATAAATTCGAAATAACCATGGTACTTTAAATGTATTTT	431
Db	1906	TTTATA	TATGTATTTAAATGTGTGTTTTATATGGTTGTATTTTTTATTTTTTTTATTATTA	1965
Qy	432	ACCA	ATTTTCCATCGAACAAACAGGTGGCTATTTTTTCGATGTGATATTTTGAATPACT	491
Db	1966	GTTT	ATATATATTTTTTATAAGAGTTGAAAGAGTTTTTTTGATGTAGGAATTTATGCTAGAGT	2025
Qy	492	AGTAC	AGGAATATCATTTGTTAGTTTGAATTTTTTAGCCCTAGAAAACAAATCGAGTTTATAGAT	551
Db	2026	TTTAG	AGAAATTTTGTGAATTTATTTGAAAGTTTATTTTATAGAAATATATGTTGTAAGTAATA	2085
Qy	552	AGCT	ATAAGTATAATTTATTTGTGATTTTAAATGGTATGGAGTTTAGGCCTATGATTAATTA	611
Db	2086	TATTTT	TTTTTTTAAAAAAAATTTATTTATTTTTTTTTTTTGTGAGAAGAGGTATTTATTTTA	2145
Qy	612	GTGAAA	ACACCCCAAGATGTTTTTATACCTTTTAAATTT	648
Db	2146	ATGAT	TTTTTTTGAAGGAGTTTATTTTTTTTTTATTTTTTTT	2182

RESULT 8	
ABU32396	
ID	ABL32396 standard; DNA; 8666 BP.
XX	
AC	ABL32396;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 369.
XX	
KW	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiarteriosclerotic; anianaemic; cytosatic; nootropic;
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW	antiinflammatory; antiarthritic; antidiabetic; antipsoriatic;
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
gs.	
XX	
OS	Homo sapiens.
XX	
PN	WO200200928-A2.
XX	
XX	03-JAN-2002.
PD	
XX	
PF	02-JUL-2001; 2001WO-EP007537.
XX	
XX	30-JUN-2000; 2000DE-01032529.
PR	01-SEP-2000; 2000DE-01043826.
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2002-130909/17.
XX	
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful for
PT	diagnosis and treatment of diseases associated with abnormal cytosine
PT	methylation.
XX	
XX	
PS	Claim 1; SEQ ID NO 369; 32pp + Sequence Listing; German.
XX	
CC	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences

CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;

Query Match 15 24; Score 106.6; DB 6; Length 8666;
Best Local Similarity 49.08; Pred. No. 2.9e-09;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

QY 12 AAAGTGTGTTTTTTTTTTCGATGATTTTAAATAAAATATCATTTTTCTTTTTTATTATTATAT 71
Db 1547 AAAGTGTGTTTTTATTATTATTAAATTTATATAATAATTTTTTAAATTTTATTATTATTA 1606

QY 72 ACTTTTAAAGTTTAAAGGTACATGTCGAAAGTGTGCAGGTAGTTACATATATATACATGT 131
Db 1607 TATTTTAAAGTTTAAAGTATATGTGTATAATGTGTAGGTTTGTATATATGTATATATGT 1666

QY 132 GCCATGCTGGTGTGCTGCACCCATTAACCTCACATGGAAGTTTTTTTTTAAATTTTAGTCACA 191
Db 1667 GTTATGTTGGTGTGTGATTATTAATTTA- TTATTTAGTATATAGGTATATTTTTTAAT 1725

QY 192 GTTTTGTAGTCATTTTCTTAATTTGAAAGTATCATTAAGTAATCATATAATTTTCAAATAAATGT 251
Db 1726 GTTATTTTGTGTTTTTTTTTTTTTATATAAGATTATTAATGGAATAATGGAATTTTAAATTTT 1785

QY 252 TAACCTACTCGATATAAAAGTTTATAGTTTCCCTACHTTTTAAGCAAAATTTCCCATAGGGCA 311
Db 1786 AGAGTAAAAATGGTTTTTATTAAGGATGTTATAATTTTTTTTAGAGTTTATTGTGAAGATAT 1845

QY 312 TGGTAATGTAGTTTCAACATTACTTCGAGTTTCAGTTAGTAAATAAATATTAAGCCTAG 371
Db 1846 GAGATATATATATTTTAAAAATTTGTTTTGGTATTTTTTAAAGTAGTTAAATTTTATATTG 1905

QY 372 TAAGTATAATTTTAATATTTGTCAAATAATTTGGAAAAATACCATGGGTACTTTAAATGATTTT 431
Db 1906 TTTTATATGATTTTAATATGTTGTTTTTATATGTTGTATTTTTTTTATTATTATTAATA 1965

QY 432 ACCAAATTTCCATGGAAACAAACAGGTGGCTATTTTTTGGATGTGATATTTTGAATACT 491
Db 1966 GTTATATATATTTTTTATAAGAGTTGAAGAGTTTTTTTGATGTAGGAATTTATGCTAGAGT 2025

QY 492 AGTACAGGAATATCATTTGTTAGTTGAATTTTTTAGCCTTAGAAAAACAATCGAGTTTAGAT 551
Db 2026 TTTTAGAGAAATTTTTTGAATTTATTTGAAGTTTTTATTTAGAAATATATGTCTAAGTGAATA 2085

QY 552 AGCTTAAAGTATAATTTATTTTGCATTTTAATAATGGTATGGAGTTAGGGCTATGATAATTA 611
Db 2086 TATTTTTTTTAAAAAAATTTATTTATTTTTTTTTTTTTTTTGGAGAAGAGGTATTTATTTTA 2145

QY 612 GTGAAACACCCCAAGAAATGTTTTATACTTTTTAAATTT 648
Db 2146 ATAGATTTTTGAAGGAGTTTATTTTTTTTTTTTATTTTTT 2182

RESULT 9
ABK34008
ID ABK34008 standard; DNA; 8666 BP.
XX AC ABK34008;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human DNA for staging of Astrocytomas #48.
XX
KW Human; ds; astrocytoma; cytostatic; staging; cysteine methylation; CpG;
KW bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
KW matrix assisted laser desorption/ionization mass spectrometry.
XX
OS Homo sapiens.

XX PN WO200202808-A2.
XX PD 10-JAN-2002.
XX PF 02-JUL-2001; 2001WO-EP007538.
XX PR 30-JUN-2000; 2000DE-01032529.
XX PR 01-SEP-2000; 2000DE-01043826.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PD WPI; 2002-171649/22.
XX PR Novel chemically modified genomic DNA sequences, useful in the
PT characterization, classification, differentiation, grading, staging,
PT treatment and/or diagnosis of astrocytomas or predisposition to
PT astrocytomas.
XX Claim 1; SEQ ID NO 95; 37pp; English.
XX The invention relates to a nucleic acid comprising a sequence (I) of at
CC least 18 bases in length of a segment of chemically pre-treated genomic
CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its
CC complement. Also included are an oligonucleotide or peptide nucleic acid
CC (or set thereof) of at least 9 nucleotides which hybridises to (I),
CC primers for (I), probes for detecting cytosine methylation or single-
CC nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide
CC nucleic acids for analysing diseases associated with the methylation
CC states of the CpG dinucleotides of (I). The array is useful for
CC determining genetic and/or epigenetic parameters, classification,
CC differentiation, grading, staging, treatment and/or diagnosis of
CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine
CC methylations, involves obtaining a biological sample containing genomic
CC DNA, extracting the genomic DNA, converting cytosine bases which are
CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or
CC another base which is dissimilar to cytosine in terms of hybridisation
CC behaviour, by chemical treatment and amplifying chemically pre-treated
CC genomic DNA fragments using the array and a polymerase, where the
CC amplificates carry a detectable label. The method further involves
CC identifying methylation status of one or more cytosine positions, and
CC analysing methylation status of the cytosine positions by reference to
CC one or more data sets. The genomic DNA is chemically treated by using a
CC bisulphite, hydrogen sulphite or disulphite. The amplification step
CC amplifies DNA which is of particular interest in astrocytoma or brain
CC tissue, based on the specific genomic methylation status of brain
CC tissues, as opposed to background DNA. The amplificates carry a
CC fluorescent label or radionuclide. Optionally, the labels of the
CC amplificates are detachable molecule fragments having a typical mass
CC which are detected in a mass spectrometer. The fragments of chemically
CC pre-treated genomic DNA to be amplified, have a single positive or
CC negative charge for a better detectability in the mass spectrometer.
CC Preferably, the amplificates or fragments of the amplificates are
CC detected by matrix assisted laser desorption/ionization mass spectrometry
CC (MALDI) or using electron spray mass spectrometry (ESI). The present
CC sequence is one of the chemically pre-treated reference DNA samples of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
Query Match 15.2%; Score 106.6; DB 6; Length 8666;
Best Local Similarity 49.0%; Pred. No. 2.9e-09;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;
QY 12 AAAGTTTTTTTTTTCATGATTAATAAATCAATTCCTTTTCTTTTATTTATTTAT 71
Db 1547 AAAGTTTTTTTTTATTAATTAATTTATATATATATTTTAAATTTTATTTATTA 1606
QY 72 ACTTTTAAGTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGT 131

Db 1607 TATTTTAAAGTTTTAGAGTATATGTGTATTAATGTGTAGGTTTGTATATATATATATGT 1666
QY 132 GCCATGCTGGTGTGTCACCCATTAACATCAATGAAGTTTTTTTTTAAATTTTAGTGACA 191
Db 1667 GTTATGTTGGTGTGTTGTTATTTAAATTTA-TTATTTAGTATTTAGGTATATTTTAAAT 1725
QY 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAATGT 251
Db 1726 GTTATTTTTTTTTTTTTTTTTTATATAAGATTTTATAATGGAATAATGGAATTTTAAATTTT 1785
QY 252 TAACTACTCTGATAAAAAAGTTTTTATAGTTTCTCTACTTTTAAAGCAAAATTTCCATAGGCA 311
Db 1786 AGAGTAAAAAGGTTTTTATTTAAGGAATGTTATTAATTTTTTTTAGAGTTTATTTAGATAT 1845
QY 312 TGGTAAATTCAGTTTCAACATTTACATTTGCAGTTTCAGTTTAGTAAATAAATTTAAGCCTAG 371
Db 1846 GAGATATATATATTTAAAAATTTGTTTTCGTATTTTAAAAAGTAGTTAAATTTTATATTTG 1905
QY 372 TAAGTATATATTTAAATTTGTCCTCAATTAATTTGGAATAATACCATGGGTACTTAATGATTT 431
Db 1906 TTTATAATGATTTTAAATGTTGTTTTATATGTTGTTATTTTATTTTATTTTATTTAATA 1965
QY 432 ACCAAATTTTCCATGGAAACAAAGGTTGGCTATTTTTTGGATTGATATTTTGAATAACT 491
Db 1966 GTTATATATATTTTATTAAGAGTTGAAGAGTTTTTGTAGTAGGAATTTATGTTAGAGT 2025
QY 492 AGTACAGGAATATCATTTGTTAGTTAGTAAATTTTACCTTAGAACCAAAATGGAGTTTAGAT 551
Db 2026 TTTAGAGAAATTTTGAATTTTATTTGAAAGTTTTTATTTAGAAAATATATGTGTAAGTGAATA 2085
QY 552 AGCTAAAGTATATTTTATTTGTTGATTTAATAATGTTATGAGTTAGGGCTATGATAATTA 611
Db 2086 TATTTTTTTTAAAAAAATTTATTTATTTTATTTTGTGAGAGAGTTATTTTATTTT 2145
QY 612 GTGAAACACCCCAAGAAATGTTTATATATTTTATTTTAAATTT 648
Db 2146 ATAGATTTTGAAGGAGTTATTTTATTTTATTTT 2182
RESULT 10
ABQ67177
ID ABQ67177 standard; DNA; 8666 BP.
AC ABQ67177;
XX
DT 28-AUG-2002 (first entry)
XX Human angiogenesis associated polynucleotide SEQ ID NO 207.
DE
XX Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
KW inflammation; rheumatoid arthritis; diabetic retinopathy; antileukemia;
KW macular degeneration; inflammatory bowel disease; Crohn's disease;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiarteriosclerotic; ds.
XX
OS Homo sapiens.
XX
XX WO200246454-A2.
XX PD 13-JUN-2002.
XX
XX 06-DEC-2001; 2001WO-EP014320.
XX
XX 06-DEC-2000; 2000DE-01061338.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Schacht O;
XX WPI; 2002-500450/53.
XX
XX New nucleic acid fragments from chemically treated angiogenesis-

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:56:58 ; Search time 192 Seconds
(without alignments)
6821.751 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_Al46311

Perfect score: 700

Sequence: 1 ctgtttcacataaagtgtttt.....gccttttagtgatgtgcca 700

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 70 summaries

Database : Issued Patents_NA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCFUS_COMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.2	16.0	601	3	US-09-949-016-77443 Sequence 77443, A
2	112.2	16.0	154626	3	US-09-949-016-14000 Sequence 14000, A
3	106.8	15.3	8766	5	US-09-984-429-354 Sequence 354, App
C 4	104.2	14.9	42595	5	US-09-984-429-469 Sequence 469, App
C 5	104	14.9	601	3	US-09-949-016-134975 Sequence 134975, A
6	104	14.9	256171	3	US-09-949-016-12822 Sequence 12822, A
7	104	14.9	256176	3	US-09-949-016-15524 Sequence 15524, A
C 8	103.8	14.8	86980	3	US-09-949-016-15344 Sequence 15344, A
C 9	102.8	14.7	260247	3	US-09-949-016-13358 Sequence 13358, A
C 10	102.6	14.7	601	3	US-09-949-002-2044 Sequence 2044, App
C 11	102.6	14.7	601	3	US-09-949-002-2045 Sequence 2045, App
C 12	102.6	14.7	18999	3	US-09-949-002-703 Sequence 703, App
C 13	102.6	14.7	26225	5	US-09-984-429-448 Sequence 448, App
C 14	102.6	14.7	27271	3	US-09-949-002-622 Sequence 622, App
C 15	102.6	14.7	360470	3	US-09-949-016-13173 Sequence 13173, A
C 16	102.4	14.6	21597	5	US-09-984-429-309 Sequence 309, App
17	102.4	14.6	194889	3	US-09-949-016-15654 Sequence 15654, A
18	101.4	14.5	325	3	US-09-513-999C-18942 Sequence 18942, A
19	101.2	14.5	69924	3	US-09-949-016-15367 Sequence 15367, A
20	101	14.4	363032	3	US-09-949-016-12415 Sequence 12415, A
21	101	14.4	363033	3	US-09-949-016-15754 Sequence 15754, A
22	100.8	14.4	181251	3	US-09-949-016-15970 Sequence 15970, A
C 23	100.8	14.4	193169	3	US-09-949-016-15091 Sequence 15091, A

RESULT 1

US-09-949-016-77443
; Sequence 77443, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77443
; LENGTH: 601

ALIGNMENTS

Sequence 426, App
Sequence 454, App
Sequence 15703, A
Sequence 16066, A
Sequence 150430, A
Sequence 13420, A
Sequence 12611, A
Sequence 14413, A
Sequence 15473, A
Sequence 13404, A
Sequence 16065, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 13276, A
Sequence 13676, A
Sequence 14374, A
Sequence 550, App
Sequence 455, App
Sequence 342, App
Sequence 15744, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 12614, A
Sequence 13027, A
Sequence 14577, A
Sequence 14578, A
Sequence 59509, A
Sequence 59510, A
Sequence 360, App
Sequence 32, Appl
Sequence 38, Appl
Sequence 13828, A
Sequence 1542, App
Sequence 13730, A
Sequence 11820, A
Sequence 17182, A
Sequence 15419, A
Sequence 13477, A
Sequence 398, App
Sequence 16151, A
Sequence 59511, A
Sequence 179319, A
Sequence 468, App
Sequence 16065, A
Sequence 13675, A
Sequence 12386, A


```
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-77443

Query Match      16.0%; Score 112.2; DB 3; Length 601;
Best Local Similarity 84.6%; Pred. No. 3.9e-13;
Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 13 AAGTTTTTTTTTTTGAATGATTTTAAATAAATATATCAATTTCTTTTTTATATATATATA 72
Db 298 AACTTTTTTTTTTTTGTGGCTTGGAAATCTTTTTTTTTTTTAAATTTTATATATATATA 357
Qy 73 CTTTAAAGTTTTTAGGGTACATGTCGAAGTGTGCAGGTTAGTTACATATATATACATGTG 132
Db 358 CTTTAAAGTTTTTAGGGTACATGTCGAACACGTGCAGGTTTGTACATATGTATACATGTG 417
Qy 133 CCATGCTGGTGTGTGTCGACCCCACTTAACCTC 161
Db 418 CCATGTTGGTGTGCTGCACCCATTAACCTC 446

RESULT 2
US-09-949-016-14000
; Sequence 14000, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14000
; LENGTH: 154626
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(154626)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14000

Query Match      16.0%; Score 112.2; DB 3; Length 154626;
Best Local Similarity 84.6%; Pred. No. 4.9e-13;
Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 13 AAGTTTTTTTTTTTGAATGATTTTAAATAAATATCAATTTCTTTTTTATATATATATA 72
Db 133339 AACTTTTTTTTTTTTGTGGCTTGGAAATCTTTTTTTTTTTTAAATTTTATATATATA 133398
Qy 73 CTTTAAAGTTTTTAGGGTACATGTCGAAGTGTGCAGGTTAGTTACATATATATACATGTG 132
Db 133399 CTTTAAAGTTTTTAGGGTACATGTCGAACACGTGCAGGTTTGTACATATGTATACATGTG 133458
Qy 133 CCATGCTGGTGTGTGTCGACCCCACTTAACCTC 161
Db 133459 CCATGTTGGTGTGCTGCACCCATTAACCTC 133487

RESULT 3
US-09-984-429-354
; Sequence 354, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 354
; LENGTH: 8766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-354

Query Match      15.3%; Score 106.8; DB 5; Length 8766;
Best Local Similarity 94.1%; Pred. No. 4.8e-12;
Matches 111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 44 TATCATTTTCTTTTTTATTATTATTATATATATCTTTTAAAGTTTATAGGGTACATGTGCAAGTG 103
Db 2 TTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 61
Qy 104 TGCAGGTAGTTACATATATATATATATATATATATATATATATATATATATATATATATAT 161
Db 62 TGCAGGTAGTTACATATATATATATATATATATATATATATATATATATATATATATATAT 119

RESULT 4
US-09-984-429-469/c
; Sequence 469, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
```



```
Matches 119; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 18 TTTTCTTTTGTGATTTTAAATAAATACATTTCTTTTATTTATTTATTTACTTTT 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89281 TTATATACCTTGTGTCATCTGTATATATTTCTTTATTTTTCATTATTATTTACTTTT 89340
Qy 78 AAGTTTGTGCTGACATGCAAGTGTGCGAGGTAGTTACATATATATATATGTCATG 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89341 AAGTTTGTGCTGACATGTCACAATGTCAGGTAGTTACATATATATATGTCATG 89400
Qy 138 CTGCTGTGCTGCACCCCAATTAACCTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89401 CTGCTGTGCTGCACCCCAATTAACCTC 89424

RESULT 8
US-09-949-016-15344/c
; Sequence 15344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15344
; LENGTH: 86980
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15344

Query Match 14.8%; Score 103.8; DB 3; Length 86980;
Best Local Similarity 81.6%; Pred. No. 2e-11;
Matches 120; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 15 GTTTTCTTTTGTGATGATTTTAAATAAATACATTTCTTTTATTTATTTATTTACT 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76334 GCITTTTATTTATTTATTTTATTTTATTTATATATATATATTTTATTTATTTACT 76275
Qy 75 TTTAAGTTTGTAGGTACATGTGCAAGTGTGCGAGTTAGTTACATATATATATGTC 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76274 TTTAAGTTTGTAGGTACATGTGCAATGTGCGAGTTAGTTACATATGTTACATGTC 76215
Qy 135 ATGCTGTGCTGCTGCACCCCAATTAACCTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76214 ATGCTGTGCTGCTGCACCCCAATTAACCTC 76188

RESULT 9
US-09-949-016-13358/c
; Sequence 13358, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 260247
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13358

Query Match 14.7%; Score 102.8; DB 3; Length 260247;
Best Local Similarity 82.3%; Pred. No. 3.3e-11;
Matches 130; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
Qy 4 TTTCACATAAAGTTTCTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTT 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93290 TTTCAATTCATAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTCA 93231
Qy 64 ATTATTATACCTTTTAAGTTTTTAGGGTACATGTGCAAGTGTGCGAGTTAGTTACATATAT 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93230 ATTATTATAC-TTTAAGTTTTTAGGGTACATGTGCAAGTGTGCGAGTTAGTTACATATGT 93172
Qy 124 ATACATGTGCCATGTGCTGTGCTGCCACCAATTAACCTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93171 GTACATGTGCCATGTGCTGTGCTGCCACCAATTAACCTC 93134

RESULT 10
US-09-949-002-2044/c
; Sequence 2044, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2044
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-2044

Query Match 14.7%; Score 102.6; DB 3; Length 601;
Best Local Similarity 86.2%; Pred. No. 2.7e-11;
Matches 125; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
Qy 17 TTTTCTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTTT 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 260 TTTTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 202
Qy 77 TAAGTTTGTAGGTACATGTGCAAGTGTGCGAGTTAGTTACATATATATATATGTCAT 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 TAAGTTTGTAGGTACATGTGCAAGTGTGCGAGTTAGTTACATATGTTACATGTCATG 142
Qy 137 GCTGTGTGCTGCTGCACCCCAATTAACCTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 GCTGTGTGCTGCTGCACCCCAATTAACCTC 117

RESULT 11
US-09-949-002-2045/c
; Sequence 2045, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
```

```
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2045
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-2045
```

```
Query Match 14.7%; Score 102.6; DB 3; Length 601;
Best Local Similarity 86.2%; Pred. No. 2.7e-11; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 19;

Qy 17 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTATTATTACTTT 76
Db 559 TTTTCTTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 501

Qy 77 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATATATACATGTGCCAT 136
Db 500 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATGTATACATGTGCCAT 441

Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161
Db 440 GCTGGTGTGCTGCACCCCAATTAATC 416
```

```
RESULT 12
US-09-949-002-703
; Sequence 703, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 18999
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-703
```

```
Query Match 14.7%; Score 102.6; DB 3; Length 18999;
Best Local Similarity 86.2%; Pred. No. 3.2e-11; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 19;

Qy 17 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTATTATTACTTT 76
Db 18674 TTTTCTTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 18732

Qy 77 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATATATACATGTGCCAT 136
Db 18733 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATGTATACATGTGCCAT 18792

Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161
Db 18793 GCTGGTGTGCTGCACCCCAATTAATC 18817
```

```
RESULT 13
US-09-984-429-448/c
; Sequence 448, Application US/09984429
```

```
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: PZ018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 448
; LENGTH: 26225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-448
```

```
Query Match 14.7%; Score 102.6; DB 5; Length 26225;
Best Local Similarity 86.2%; Pred. No. 3.2e-11; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 19;

Qy 17 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTATTATTACTTT 76
Db 9503 TTTTCTTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 9445

Qy 77 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATATATACATGTGCCAT 136
Db 9444 TAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATGTATACATGTGCCAT 9385

Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161
Db 9384 GCTGGTGTGCTGCACCCCAATTAATC 9360
```

```
RESULT 14
US-09-949-002-622
; Sequence 622, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622
; LENGTH: 27271
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-622

Query Match 14.7%; Score 102.6; DB 3; Length 27271;
```


Db 107969 TAC-TTAAAGTTTGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATG 108027
Qy 131 TGCCATGCTGGTGTGCTGCACCCATTAACTC-ACATGAAGTTTCTTTAAATTTTAGTGA 189
Db 108028 TGCCATGCTGCTGCACCTGCACCCCACTACTCGTCACTAGCATTAATTTAAATTTGTTTA 108087
Qy 190 CAGTTTGTAGTCA 201
Db 108088 GTTTTTTTTGA 108099

RESULT 18
US-09-513-999C-18942
; Sequence 18942, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18942
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 124.
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 127
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 143
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 308
; OTHER INFORMATION: n=a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: 309
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-18942

Query Match 14.5%; Score 101.4; DB 3; Length 325;
Best Local Similarity 83.7%; Pred. No. 4.6e-11;
Matches 108; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Qy 33 TTTTAATAAATATACATTTCTTTTTTATTATTATTATTTTAAAGTTTGGGTACA 92
Db 86 TTTTATTATGTTAACTTTTTTTTAAATTATTATAAATTTAAAGTTTGGGTACA 145
Qy 93 TGTGCAAGTGTGCAAGGTTAGTTACATATATACATGTGCATGCTGGTGTGCACC 152
Db 146 TGTGCWCAATGTCAGGTTAGTTACATATATATATGTGCATGCTGGTGTGCACC 205

Qy 153 CATTAACCTC 161
Db 206 CATTAACCTC 214

RESULT 19
US-09-949-016-15367
; Sequence 15367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15367
; LENGTH: 69924
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15367

Query Match 14.5%; Score 101.2; DB 3; Length 69924;
Best Local Similarity 81.6%; Pred. No. 6.3e-11;
Matches 129; Conservative 0; Mismatches 28; Indels 1; Gaps 1;
Qy 4 TTTCCACATAAAGTTTTTTTTTTTCATGATTTTAAATAAAATATCATTTCTTTTTTATT 63
Db 49733 TTTAGTTTATAGCTTGTAACTTTCATTTATTTTATTTTATTTTATTTTATT 49792
Qy 64 ATTATTATACCTTTTAAGTTTGGGTACATGTCACCAAGTGTGCAGGTAGTTACATATAT 123
Db 49793 ATTATTATACCTTT-AAAGTTTGGGTACATGTCACCAATGTCAGGTAGTTACATATGT 49851
Qy 124 ATACATGTGCCATGCTGCTGTGCTGCACCCCACTAACTC 161
Db 49852 ATACATGTGCCATGCTGCTGTGCTGCACCCCACTAACTC 49889

RESULT 20
US-09-949-016-12415
; Sequence 12415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12415
; LENGTH: 363032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature

```
; LOCATION: (1)...(363032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12415

Query Match      14.4%; Score 101; DB 3; Length 363032;
Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 14 AGTTTTTTTTTTGATGATTTTAATAAAATATCATTTCTTTTTTATTATTATTATAC 73
Db 76601 AATTTTTTTTTTGTGCTCGCAATTTCTTTCTTTTTTTTTTTTTTTAAATATA 76660

QY 74 TTTTAAGTTTTAGGTCATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGC 133
Db 76661 CTTTAAAGTTTTAGGTCATGTGCACATTTGTGCAGGTTAGTTACATATGTGC 76720

QY 134 CATGCTGGTGTGCTGCCACCCCACTAACTCA 162
Db 76721 CATGCTGGTGTGCTGCCACCCCACTAACTCA 76749

RESULT 21
US-09-949-016-15754
; Sequence 15754, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15754
; LENGTH: 363033
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(363033)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15754

Query Match      14.4%; Score 101; DB 3; Length 363033;
Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 14 AGTTTTTTTTTTGATGATTTTAATAAAATATCATTTCTTTTTTATTATTATTATAC 73
Db 76601 AATTTTTTTTTTGTGCTCGCAATTTCTTTCTTTTTTTTTTTTTTTAAATATA 76660

QY 74 TTTTAAGTTTTAGGTCATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGC 133
Db 76661 CTTTAAAGTTTTAGGTCATGTGCACATTTGTGCAGGTTAGTTACATATGTGC 76720

QY 134 CATGCTGGTGTGCTGCCACCCCACTAACTCA 162
Db 76721 CATGCTGGTGTGCTGCCACCCCACTAACTCA 76749

RESULT 22
US-09-949-016-15970
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15970

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15970

Query Match      14.4%; Score 100.8; DB 3; Length 181251;
Best Local Similarity 64.5%; Pred. No. 7.8e-11;
Matches 182; Conservative 0; Mismatches 97; Indels 3; Gaps 2;

QY 16 TTTTTTTTTTTGATGATTTTAATAAAATATCATTTCTTTTTTATTATTATTACTT 75
Db 75583 TTCTTTTTTTTATTATTAAAGTTTTTTTAAAAATTAATTTAGTATTATTATAC-T 75641

QY 76 TTAAGTTTTAGGTCATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db 75642 TTAAGTTTTAGGTCATGTGCACAAATGTGCAGGTTAGTTACATATGTACATGTGCCA 75701

QY 136 TGCTGGTGTGCTGCCACCCCACTAACTCACAATGAGTTTTTTTAAATTTAGTCACAGTTT 195
Db 75702 TGCTGGTGTGCTGCCACCCCACTAGGACATGGATGAAATGGAAATCATCTCTACTA 75761

QY 196 TAGTCATTTTCTCTAAATTGAAAGTATCATAAATCCATAAATTTGAAAAAATGTTAAC 255
Db 75762 AACTCGTTTTGTCTCTAAAGAAT--TTAGGACATGTTATTTTGGAGACTGTTTTTACA 75819

QY 256 TACTCTGATAAAAAAGTTTTTATAGTTTCTCTACTTTTAAAGCAA 297
Db 75820 TTTGATTATGGATGCATTTTATAGTTGTTTAAATCTTTGGCTA 75861

RESULT 23
US-09-949-016-15091/c
; Sequence 15091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15091
; LENGTH: 193169
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15091
```



```
Query Match      14.4%; Score 100.8; DB 3; Length 193169;
Best Local Similarity 81.2%; Pred. No. 7.8e-11;
Matches 117; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 19 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTATCTTTA 78
Db 21017 TTATTGTTTGTGTTTATACCGTATTTACTATTCTTTTTTTTTTTTATACCTTTA 20958

QY 79 AGTTTTAGGTTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGC 138
Db 20957 AGTTTTAGGTTACATGTGCAACAGTGCAGGTTGTTACATATGTATACATGTGCCATGT 20898

QY 139 TGGTGTGTGCACCACTAACTCA 162
Db 20897 TGGTGTGTGTACCCCACTAACTCA 20874

RESULT 24
US-09-984-429-426/c
; Sequence 426, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 426
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-426

Query Match      14.3%; Score 100.4; DB 5; Length 1055;
Best Local Similarity 84.9%; Pred. No. 7.5e-11;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTATCTTT 75
Db 1038 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAC-T 980

QY 76 TTAAGTTTTAGGTTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db 979 TTAAGTTTTAGGTTACATGTGCAACATGTGCAGGTTAGTGACATGTGTATACATGTGCCA 920

QY 136 TCGTGGTGTGCTGCCACCACTAACTC 161
Db 919 TCGTGGTGTGCTGCCACCACTAACTC 894

RESULT 26
US-09-949-016-15703/c
; Sequence 15703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15703
; LENGTH: 91538
; TYPE: DNA
; ORGANISM: Human
```

```
Query Match      14.4%; Score 100.8; DB 3; Length 193169;
Best Local Similarity 81.2%; Pred. No. 7.8e-11;
Matches 117; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 19 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTATCTTTA 78
Db 21017 TTATTGTTTGTGTTTATACCGTATTTACTATTCTTTTTTTTTTTTATACCTTTA 20958

QY 79 AGTTTTAGGTTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGC 138
Db 20957 AGTTTTAGGTTACATGTGCAACAGTGCAGGTTGTTACATATGTATACATGTGCCATGT 20898

QY 139 TGGTGTGTGCACCACTAACTCA 162
Db 20897 TGGTGTGTGTACCCCACTAACTCA 20874

RESULT 24
US-09-984-429-426/c
; Sequence 426, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 426
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-426

Query Match      14.3%; Score 100.4; DB 5; Length 1055;
Best Local Similarity 84.9%; Pred. No. 7.5e-11;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTATCTTT 75
Db 1038 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAC-T 980

QY 76 TTAAGTTTTAGGTTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db 979 TTAAGTTTTAGGTTACATGTGCAACATGTGCAGGTTAGTGACATGTGTATACATGTGCCA 920

QY 136 TCGTGGTGTGCTGCCACCACTAACTC 161
Db 919 TCGTGGTGTGCTGCCACCACTAACTC 894

RESULT 25
US-09-984-429-454/c
; Sequence 454, Application US/09984429
```

US-09-949-016-15703

Query Match 14.3%; Score 100.4; DB 3; Length 91538;
Best Local Similarity 84.9%; Pred. No. 9e-11;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTTACTT 75
DB 23790 TTTATTATTATTAAATTTTATTATTATTATTATTATTATTATTATTATTATTAT 23732

QY 76 TTAAGTTTTAGGGTACATGTCGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 23731 TTAAGTTTTAGGGTACATGTCGCAATGTGCAGGTTAGTTACATATGTATACATGTGCCA 23672

QY 136 TGTGTGTGTGTCGACCCCACTTAACCTC 161
DB 23671 TGTGTGTGTCGTCGACCCCACTTAACCTC 23646

RESULT 27

US-09-949-016-16066/c
; Sequence 16066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16066
; LENGTH: 144362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(144362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16066

Query Match 14.3%; Score 100.4; DB 3; Length 144362;
Best Local Similarity 82.5%; Pred. No. 9.2e-11;
Matches 127; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 9 CATAAAGTTTTTTTTTTCATGATGATTTTAAATAAATATCATTTCTTTTATTATTAT 68
DB 26372 CAGAAGCTCTCTTTATTATTATTATGATGATGATGATTTATTATTATTAT 26313

QY 69 TATACCTTTTAAGTTTAAAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATATATACA 128
DB 26312 TATAC-TTTAAGTTTAAAGGTACATGTCGCAATGTGCAGGTTAGTTACATATATACA 26254

QY 129 TGTGCCATGCTGCTGTCGACCCCACTTAACCTCA 162
DB 26253 TGTGCCATGCTGCTGTCGACCCCACTTAACCTCA 26220

RESULT 28

US-09-949-016-150430
; Sequence 150430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150430
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150430

Query Match 14.3%; Score 100.2; DB 3; Length 601;
Best Local Similarity 71.2%; Pred. No. 8e-11;
Matches 146; Conservative 0; Mismatches 58; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACTT 75
DB 380 TTTCTTTTTTTTATTATTAAAGTTTTTTTTTAAATTTTATTAGTATTATTATAC-T 438

QY 76 TTAAGTTTTAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 439 TTAAGTTTTAGGTACATGTCGCAATGTGCAGGTTAGTTACATATGTATACATGTGCCA 498

QY 136 TGTGTGTGTGTCGACCCCACTTAACCTCACTGAAGTTTTTTTTTAAATTTTAGTCACAGTTT 195
DB 499 TGTGTGTGTGTCGACCCCACTTAGGCACATGGATGAAATTTGGAATCATCTTCACTA 558

QY 196 TAGTCATTTTCCTTAATTGAAAGTAT 220
DB 559 AACTGCTTTTGTGTTTCTTAAAGAAAT 583

RESULT 29

US-09-949-016-13420
; Sequence 13420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13420
; LENGTH: 47363
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(47363)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13420

Query Match 14.3%; Score 100.2; DB 3; Length 47363;
Best Local Similarity 81.5%; Pred. No. 9.6e-11;
Matches 128; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 5 TTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTCTTTTATTATTA 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


```
Db 321248 CATTAACCTC 321256

RESULT 33
US-09-949-016-13404
; Sequence 13404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13404
; LENGTH: 237863
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13404

Query Match 14.3%; Score 100; DB 3; Length 237863;
Best Local Similarity 80.6%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 2 TGTTCACATAAGATTTTTCCTGATGATTTTAAATAAATATCATCTTCTTTTAA 61
Db 154366 TGTACATATCAGACGCTGTTTTCTGTTGTTGTTGTTGTTGTTTATTT 154425

Qy 62 TTATTATTATCTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTACAT 121
Db 154426 TTATTATTATGC-TTTAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTACAT 154484

Qy 122 ATATACATGTGCCATGCTGCTGCTGCACCCCAATTAACCTC 161
Db 154485 GCATACATGTGCCATGCTGCTGCTGTACCCCAATTAACCTC 154524

RESULT 34
US-09-949-016-16065/c
; Sequence 16065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16065
; LENGTH: 212139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16065

Query Match 14.3%; Score 99.8; DB 3; Length 212139;
Best Local Similarity 81.1%; Pred. No. 1.2e-10;
Matches 116; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 321248 CATTAACCTC 321256

Qy 18 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTCTTTTATTTATTTATTTATTT 77
Db 125374 TTATCTACTTGTAGTCTCCACTTGGATTTCTTTTTTTTATTTATTTATTTATTTATTT 125315

Qy 78 AAGTTTTCAGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATG 137
Db 125314 AAGTTTTCAGGTACATGTGCAACACGTCGCAACTTTGTTACATATGTATACATGTGCCATG 125255

Qy 138 CTGGTGTGCTGCACCCCAATTAACCT 160
Db 125254 TTGGTATGCTGCACCCCAATTAACCT 125232

RESULT 35
US-09-245-041-16/c
; Sequence 16, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-041-16

Query Match 14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTATTTATTTATTTATTTACTT 75
Db 4066 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTATTTATTTATTTATTTACTT 4007

Qy 76 TTAAGTTTTCAGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 4006 TTAAGTTTTCAGGTACATGTGCAACACATGCAGGTTTGTACATATGTATACATATGCCA 3947

Qy 136 TCGTGTGCTGCACCCCAATTAACCTC 161
Db 3946 TGTGTGTGCTGCACCCCAATTAACCTC 3921

RESULT 36
US-09-358-055B-16/c
; Sequence 16, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D. L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
```

```
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-358-055B-16

Query Match      14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGAGTATTAAATAAATATACATTTCTTTTATTTATTTATTTATTTACTT 75
Db 4066 TTTTCTTTTGTGAGTATTAAATAAATATACATTTCTTTTATTTATTTATTTATTTACTT 4007

QY 76 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTAGTTACATATATATACATGTGCCA 135
Db 4006 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTTGTACATATGTATACATATGCCA 3947

QY 136 TCGTGGTGTGTCGACCCCAATTAACTC 161
Db 3946 TGTGGTGTGTCGACCCCAATTAACTC 3921

RESULT 37
US-09-893-238-16/c
; Sequence 16, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagie, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-893-238-16

Query Match      14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGAGTATTAAATAAATATACATTTCTTTTATTTATTTATTTATTTACTT 75
Db 4066 TTTTCTTTTGTGAGTATTAAATAAATATACATTTCTTTTATTTATTTATTTATTTACTT 4007

QY 76 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTAGTTACATATATATACATGTGCCA 135
Db 4006 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTTGTACATATGTATACATATGCCA 3947

QY 136 TCGTGGTGTGTCGACCCCAATTAACTC 161
Db 3946 TGTGGTGTGTCGACCCCAATTAACTC 3921

RESULT 38
US-09-949-016-13276/c
; Sequence 13276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14374
; LENGTH: 112623
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112623)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14374

Query Match      14.2%; Score 99.6; DB 3; Length 112623;
Best Local Similarity 83.3%; Pred. No. 1.3e-10;
Matches 125; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

QY 12 AAAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTAT 71
Db 125 AAAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTAT 71
```



```
Db 4895 -TAAAGTTTGGGTACATGTGCACAATGTGCAGGTAGTCACATATGTATACATGTGCCA 4837
      |||
Qy 136 TGCTGGTGTGCTGCACCCATTAAC 160
      |||
Db 4836 TGCTGGTGTGCTGCACCCATTAAC 4812
      |||

RESULT 43
US-09-949-016-15744
; Sequence 15744, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15744
; LENGTH: 64049
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15744

Query Match 14.2%; Score 99.4; DB 3; Length 64049;
Best Local Similarity 80.1%; Pred. No. 1.4e-10;
Matches 129; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Qy 2 TGTTTCACATAAAGTTTTTTTTTTTGGTGAATTTTAAATAAATATCATTTCTTTTTTA 61
      |||
Db 50324 TGAGTTACAAAAGTTTTTAACTTTTATGTTAAAGATTATTATTATTATTATTA 50383
      |||

Qy 62 TTATTATTACTTTTAAAGTTTTTAGGTACATGTGCACCAAGTGTGCAGGTAGTTACATAT 121
      |||
Db 50384 TTATTATTATAC-TTTAAGTTTTTAGGTACATGTGCACCAAGTGTGCAGGTAGTTACATAT 50442
      |||

Qy 122 ATATACATGTCGCATGCTGCTGCACCACTTAAC 162
      |||
Db 50443 GTATACATGTCGCATGCTGCTGCACCACTTAAC 50483
      |||

RESULT 44
US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. 6537780
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001192
; CURRENT APPLICATION NUMBER: US/09/818,512
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 116592
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3
```

```
Query Match 14.2%; Score 99.4; DB 3; Length 116592;
Best Local Similarity 82.4%; Pred. No. 1.4e-10;
Matches 126; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Qy 6 TCACATAAAGTTTTTTTTTTTGGTGAATTTTAAATAAATATCATTTCTTTTTTATTAT 65
      |||
Db 48471 TCAGAAAAATATATTTTTTTTTTTCATTTATTTTATTTATTTATTTATTTT 48530
      |||

Qy 66 TATTATACCTTTTAAAGTTTTTAGGTACATGTGCACCAAGTGTGCAGGTAGTTACATATAT 125
      |||
Db 48531 TATTATACCTC-TAAGTTTTTAGGTACATGTGCACATTTGTGCAGGTAGTTACATATAT 48589
      |||

Qy 126 ACATGTGCCATGCTGGTGTGCTGCACCCACTAA 158
      |||
Db 48590 ACATGTGCCATGCTGGTGTGCTGCACCCACTAA 48622
      |||

RESULT 45
US-10-354-065-3
; Sequence 3, Application US/10354065
; Patent No. 6884609
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001192DIV
; CURRENT APPLICATION NUMBER: US/10/354,065
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 116592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-10-354-065-3

Query Match 14.2%; Score 99.4; DB 3; Length 116592;
Best Local Similarity 82.4%; Pred. No. 1.4e-10;
Matches 126; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Qy 6 TCACATAAAGTTTTTTTTTTTGGTGAATTTTAAATAAATATCATTTCTTTTTTATTAT 65
      |||
Db 48471 TCAGAAAAATATATTTTTTTTTTTCATTTATTTTATTTATTTATTTATTTT 48530
      |||

Qy 66 TATTATACCTTTTAAAGTTTTTAGGTACATGTGCACCAAGTGTGCAGGTAGTTACATATAT 125
      |||
Db 48531 TATTATACCTC-TAAGTTTTTAGGTACATGTGCACATTTGTGCAGGTAGTTACATATAT 48589
      |||

Qy 126 ACATGTGCCATGCTGGTGTGCTGCACCCACTAA 158
      |||
Db 48590 ACATGTGCCATGCTGGTGTGCTGCACCCACTAA 48622
      |||

RESULT 46
US-09-949-016-12614/c
; Sequence 12614, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12614
; LENGTH: 248968
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(248968)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12614

Query Match 14.2%; Score 99.2; DB 3; Length 248968;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 22 TTTTTCATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTATTTAAAGT 81
DB 163938 TTTTCTTTCTTTTAAATTAATTTATTTTATTTATTTATTTATTTATTTAAAGT 163880
SEQ ID NO 12614
LENGTH: 248968
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(248968)
OTHER INFORMATION: n = A,T,C or G

QY 82 TTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGG 141
DB 163879 TTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGG 163820

QY 142 TGTGCTGCACCCATTAACTC 161
DB 163819 TGTACTGCACCCATTAACTC 163800

RESULT 47

US-09-949-016-16061/c
; Sequence 16061, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16061
; LENGTH: 250958
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(250958)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16061

Query Match 14.2%; Score 99.2; DB 3; Length 250958;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 22 TTTTTCATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTATTTAAAGT 81
DB 213928 TTTTCTTTCTTTTAAATTAATTTATTTTATTTATTTATTTATTTATTTAAAGT 213870
SEQ ID NO 16061
LENGTH: 250958
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(250958)
OTHER INFORMATION: n = A,T,C or G

QY 82 TTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGG 141
DB 213869 TTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGG 213810

QY 142 TGTGCTGCACCCATTAACTC 161
DB 213809 TGTACTGCACCCATTAACTC 213790

RESULT 48
US-09-949-016-13027/c
; Sequence 13027, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13027
; LENGTH: 45138
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(45138)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13027

Query Match 14.1%; Score 99; DB 3; Length 45138;
Best Local Similarity 88.1%; Pred. No. 1.6e-10;
Matches 119; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 27 TGTGATTTTAAATAATATCATTTCTTTTATTTATTTATTTATTTATTTAAAGTTTAG 86
DB 30469 TAACAATATTAATTTATTTCTTTTATTTATTTATTTATTTATTTATTTATTTAC 30411
SEQ ID NO 13027
LENGTH: 45138
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(45138)
OTHER INFORMATION: n = A,T,C or G

QY 87 GGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGGTGTGC 146
DB 30410 GGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTGGTGTGC 30351

QY 147 TGCACCCATTAACTC 161
DB 30350 TGCACCCATTAACTC 30336

RESULT 49

US-09-949-016-14577
; Sequence 14577, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14577
; LENGTH: 678533
; TYPE: DNA

Query Match 14.2%; Score 99.2; DB 3; Length 250958;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 22 TTTTTCATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTATTTAAAGT 81
DB 213928 TTTTCTTTCTTTTAAATTAATTTATTTTATTTATTTATTTATTTATTTAAAGT 213870
SEQ ID NO 14577
LENGTH: 678533
TYPE: DNA

[illegible]

US-09-949-016-11820

Query Match 14.1%; Score 98.8; DB 3; Length 192700;
 Best Local Similarity 84.2%; Pred. No. 1.9e-10;
 Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTT 75
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132478 TTTTCTTTTTCATGATTTTAAACACCTCAAACTTTTATTTATTTATTTATAC-T 132420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132419 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTAGTTACATATATATACATGTGCCA 132360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 136 TGTGTGTGTGTCACCCCAATTAATC 161
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132359 TGTGTGTGCACTGCACCCCAATTAATC 132334
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 60
 US-09-949-016-17182/c
 ; Sequence 17182, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17182
 ; LENGTH: 192704
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-17182

Query Match 14.1%; Score 98.8; DB 3; Length 192704;
 Best Local Similarity 84.2%; Pred. No. 1.9e-10;
 Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTT 75
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132478 TTTTCTTTTTCATGATTTTAAACACCTCAAACTTTTATTTATTTATTTATAC-T 132420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132419 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTAGTTACATATATATACATGTGCCA 132360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 136 TGTGTGTGTGTCACCCCAATTAATC 161
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 132359 TGTGTGTGCACTGCACCCCAATTAATC 132334
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 61
 US-09-949-016-15419
 ; Sequence 15419, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15419
 ; LENGTH: 192704
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-15419

Query Match 14.1%; Score 98.8; DB 3; Length 232024;
 Best Local Similarity 83.8%; Pred. No. 1.9e-10;
 Matches 124; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

QY 17 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTT 74
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 82901 TCTTTTTTTTAAATAAATAATTTATTTATTTATTTATTTATTTATTTATAGAC 82960
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 75 TTTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCC 134
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 82961 TTTAAGTTTATAGGTACATGTGCACATGTGCAGGTAGTTACATATATATACATGTGCC 83020
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 135 ATGCTGTGTGTCACCCCAATTAATC 162
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

[illegible]

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 07:08:31 ; Search time 1464 Seconds
(without alignments)
5875.235 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_A146311

Perfect score: 700

Sequence: 1 ctgtttcacataaagttttt.....gccttttaggtggtggca 700

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 70 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	699.6	100.0	190276	10	US-10-661-966-1
c 2	113.2	16.2	19167	3	Sequence 1, Appli
3	109.2	15.6	100364	9	Sequence 8028, Ap
c 4	107	15.3	563	6	Sequence 6776, Ap
c 5	107	15.3	563	7	Sequence 267263,
6	107	15.3	596	4	Sequence 267263,
7	107	15.3	596	5	Sequence 728921,
8	106.8	15.3	8766	3	Sequence 728921,
9	106.6	15.2	8666	7	Sequence 354, App
10	106.6	15.2	8666	8	Sequence 369, App
11	106.6	15.2	8666	8	Sequence 27, Appl
12	106.6	15.2	8666	8	Sequence 95, Appl
c 13	105.8	15.1	493	4	Sequence 207, App
c 14	105.8	15.1	493	4	Sequence 477191,
c 15	105.8	15.1	493	5	Sequence 477191,
c 16	105.8	15.1	498	6	Sequence 267266,
c 17	105.8	15.1	498	7	Sequence 267266,
c 18	105.8	15.1	563	6	Sequence 267262,

ALIGNMENTS

RESULT 1

- US-10-661-966-1
- ; Sequence 1, Application US/10661966
- ; Publication No. US20050277118A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Roth, Richard B.
- ; APPLICANT: Nelson, Matthew Roberts
- ; APPLICANT: Braun, Andreas
- ; TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBJECTS AT RISK
- ; TITLE OF INVENTION: OF MELANOMA AND TREATMENTS THEREOF
- ; FILE REFERENCE: 524592003800
- ; CURRENT APPLICATION NUMBER: US/10/661,966
- ; PRIOR FILING DATE: 2003-09-11
- ; PRIOR FILING DATE: 2002-09-11

- Sequence 267262,
- Sequence 4, Appli
- Sequence 267264,
- Sequence 267265,
- Sequence 267264,
- Sequence 267265,
- Sequence 235941,
- Sequence 235942,
- Sequence 235943,
- Sequence 235941,
- Sequence 235942,
- Sequence 235943,
- Sequence 3, Appli
- Sequence 3, Appli
- Sequence 578850,
- Sequence 1192259,
- Sequence 51, Appl
- Sequence 214, App
- Sequence 321, App
- Sequence 6940, Ap
- Sequence 564441,
- Sequence 1177850,
- Sequence 469, App
- Sequence 238, App
- Sequence 98, Appl
- Sequence 19, Appl
- Sequence 1330, Ap
- Sequence 17645, A
- Sequence 13253, A
- Sequence 577167,
- Sequence 1190576,
- Sequence 3, Appli
- Sequence 12101, A
- Sequence 661, App
- Sequence 661, App
- Sequence 661, App
- Sequence 76, Appl
- Sequence 570607,
- Sequence 1184016,
- Sequence 552761,
- Sequence 1166170,
- Sequence 256997,
- Sequence 256998,
- Sequence 256997,
- Sequence 256998,
- Sequence 91798, A
- Sequence 91799, A
- Sequence 705207,
- Sequence 705208,
- Sequence 83, Appl
- Sequence 1276, Ap
- Sequence 448, App
- Sequence 1276, Ap

```
; PRIOR APPLICATION NUMBER: 60/422,344
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 190276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-661-966-1

Query Match      100.0%; Score 700; DB 10; Length 190276;
Best Local Similarity 99.9%; Pred. No. 4.5e-118;
Matches 699; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAATAATACATTTCTTTTTT 60
DB 146001 CTGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAATAATACATTTCTTTTTT 146060

QY 61 ATTATTATTATACCTTTTAAGTTTGTAGGTACATGTCGAAAGTGTGCAGGTAGTTACATA 120
DB 146061 ATTATTATTATACCTTTTAAGTTTGTAGGTACATGTCGAAAGTGTGCAGGTAGTTACATA 146120

QY 121 TATATACATGTGCCATGCTGCTGTGCTGCCACCACTTAACATCAATGATGATTTTAA 180
DB 146121 TATATACATGTGCCATGCTGCTGTGCTGCCACCACTTAACATCAATGATGATTTTAA 146180

QY 181 TTTTAGTGACAGTTTGTAGTCATTTTCTTAATTTGAAAGTATCATAGTAATCCATAATTT 240
DB 146181 TTTTAGTGACAGTTTGTAGTCATTTTCTTAATTTGAAAGTATCATAGTAATCCATAATTT 146240

QY 241 GAAAAAATCTTAACACTCTCGATAAAAAAGTTTATAGTTTCTCTACTTTTAAGCAAAAT 300
DB 146241 GAAAAAATCTTAACACTCTCGATAAAAAAGTTTATAGTTTCTCTACTTTTAAGCAAAAT 146300

QY 301 TCCATAGGGCATGTGTAATTTGTAGTTTCAACATTTACATTTGCAAGTTTCAGTTAGTAAATAAT 360
DB 146301 TCCATAGGGCATGTGTAATTTGTAGTTTCAACATTTACATTTGCAAGTTTCAGTTAGTAAATAAT 146360

QY 361 ATTAAGCTTAGTAAATTAATTTAATTTGTCAAATTAATTTGGAATAATCCATGGGTACT 420
DB 146361 ATTAAGCTTAGTAAATTAATTTAATTTGTCAAATTAATTTGGAATAATCCATGGGTACT 146420

QY 421 TAATTGATTTTACCAATTTTCCATGGGAACAAAGTTGCGTATTTTGGGATTCATAT 480
DB 146421 TAATTGATTTTACCAATTTTCCATGGGAACAAAGTTGCGTATTTTGGGATTCATAT 146480

QY 481 TTTGAAATACCTAGTACAGGAATATCATTTGTAGTTGAATTTTGTAGCTTGAAGAAACAAAT 540
DB 146481 TTTGAAATACCTAGTACAGGAATATCATTTGTAGTTGAATTTTGTAGCTTGAAGAAACAAAT 146540

QY 541 GGAGTTTAGATAGCTAAAGTATAATTTATTTGTGATTTAATTAATGATGAGTTAGGCG 600
DB 146541 GGAGTTTAGATAGCTAAAGTATAATTTATTTGTGATTTAATTAATGATGAGTTAGGCG 146600

QY 601 TATGATAATTTAGTGAACCAACCCCAAGAAATGTTTATATCTTTTAAATTTTAAATAATTCGAAA 660
DB 146601 TATGATAATTTAGTGAACCAACCCCAAGAAATGTTTATATCTTTTAAATTTTAAATAATTCGAAA 146660

QY 661 TGACACTTGGAGTAACAAATTCCTTTTGTAGGTGATGGCA 700
DB 146661 TGACACTTGGAGTAACAAATTCCTTTTGTAGGTGATGGCA 146700

RESULT 2
US-09-764-891-8028/c
; Sequence 8028, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
```

```
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8028
; LENGTH: 19167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8028

Query Match      16.2%; Score 113.2; DB 3; Length 19167;
Best Local Similarity 82.3%; Pred. No. 1.5e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 TTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAATAATCATTTCTTTTTTATT 63
DB 10109 TTATAACTAACTTTTTTTTTTTTGTGCTTGGAAATCTTTTTTTTAAATTTATT 10050

QY 64 ATTATTATATCTTTTAAGTTTGTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATAT 123
DB 10049 ATTATTATATCTTTTAAGTTTGTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATAT 9990

QY 124 ATACATGTGCCATGTGCTGTGCTGCCACCACTTAATCTC 161
DB 9989 ATACATGTGCCATGTGCTGTGCTGCCACCACTTAATCTC 9952

RESULT 3
US-10-719-993-6776
; Sequence 6776, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6776
; LENGTH: 100364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(100364)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-719-993-6776

Query Match      15.6%; Score 109.2; DB 9; Length 100364;
Best Local Similarity 84.2%; Pred. No. 1.4e-09;
Matches 123; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 23 TTTTGTGATGATTTTAATAAATAATCATTTTCTTTTTTATTATTATATATATCTTTTAAGTT 82
DB 30826 TTCTTTTTTTTTTTTAACTTTTAAATTTTAAATTTATTTATATATCTTTTAAGTT 30885

QY 83 TTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTCGCAATGCTGGT 142
DB 30886 TTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTCGCAATGCTGGT 30945

QY 143 GTGCTGCACCCCACTTAATCTCACATGAA 168
DB 30946 GTGCTGCACCCCACTTAATCTCCCGAA 30971

RESULT 4
US-10-027-632-267263/c
; Sequence 267263, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267263
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263
```

```
Query Match 15.3%; Score 107; DB 6; Length 563;
Best Local Similarity 65.8%; Pred. No. 6.5e-10;
Matches 185; Conservative 1; Mismatches 91; Indels 4; Gaps 2;

Qy 12 AAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTAT 71
Db 455 AATATTATATACATATTTAAATATGTTATTATTCAATATCTTTTATTATTAT 396

Qy 72 ACTTTTAAGTTTGGGTACATGTCGCAAGTGTGCAGTTAGTTACATATATACATGT 131
Db 395 AC-TTTAAGTTTGGGTACATGTCGCAATGTGCAGTTAGTTACATATACATGT 337

Qy 132 GCCATGCTGGTGTGCTGCACCCATTAACTCAGTCAATGTTTAAATTTTAGTGACA 191
Db 336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCAATTAGCATTTAGGTATCTCCTTA 280

Qy 192 GTTTTAGTCATTTTCCCTAAATGAAAGTATCATTAAGTAATCCATAAATTTGAAAAAATGT 251
Db 279 ATGCTATCCCTCCCTTATTAATATTTCTTATGTCATAAATATATTATTATAAATGT 220

Qy 252 TAACACTCTCGATAAAAAAGTTTATAGTTTCCCTACTTTTA 292
Db 219 TTTCTGTTTAAATATGTTATTATTCATGTTTAGTGTTT 179
```

```
RESULT 5
US-10-027-632-267263/c
; Sequence 267263, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267263
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263
```

```
Query Match 15.3%; Score 107; DB 7; Length 563;
Best Local Similarity 65.8%; Pred. No. 6.5e-10;
Matches 185; Conservative 1; Mismatches 91; Indels 4; Gaps 2;

Qy 12 AAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTAT 71
Db 455 AATATTATATACATATTTAAATATGTTATTATTCAATATCTTTTATTATTAT 396

Qy 72 ACTTTTAAGTTTGGGTACATGTCGCAAGTGTGCAGTTAGTTACATATATACATGT 131
Db 395 AC-TTTAAGTTTGGGTACATGTCGCAATGTGCAGTTAGTTACATATATACATGT 337

Qy 132 GCCATGCTGGTGTGCTGCACCCATTAACTCAGTCAATGTTTAAATTTTAGTGACA 191
Db 336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCAATTAGCATTTAGGTATCTCCTTA 280

Qy 192 GTTTTAGTCATTTTCCCTAAATGAAAGTATCATTAAGTAATCCATAAATTTGAAAAAATGT 251
Db 279 ATGCTATCCCTCCCTTATTAATATTTCTTATGTCATAAATATATTATTATAAATGT 220

Qy 252 TAACACTCTCGATAAAAAAGTTTATAGTTTCCCTACTTTTA 292
Db 219 TTTCTGTTTAAATATGTTATTATTCATGTTTAGTGTTT 179
```

```
RESULT 6
US-09-925-065A-728921
; Sequence 728921, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 728921
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-728921
```

```
Query Match 15.3%; Score 107; DB 4; Length 596;
Best Local Similarity 83.0%; Pred. No. 6.6e-10;
Matches 122; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 15 GTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACT 74
Db 325 GTTCTTTTCTTTTAAATATTTTATTATTATTATAAATATTATTACT 384
```


Db 1667 GTTATGTTGGTGTGTTATTAATTAATTA - TTATTTAGTATTAGGTATATATTTTAAAT 1725
Qy 192 GTTTTAGTCATTTTCCATAATGAAGTATCATAGTATCATTAATCCATAAATTTGAAAAAATGT 251
Db 1726 GTTATTTTATTTTATTTTATTAAGATTTTATAAGATTTTATAAGTATGATGATTTTAAATTTT 1785
Qy 252 TAACCTACTCTGATAAAAAAGTTTATAGTTTTCCTACTTTTAAAGCAAAATTCATAGGGCA 311
Db 1786 AGAGTAAATGGTTTATTTAAGGATGTTATAATTTTATAGAGTTTATTTGTAAGATAT 1845
Qy 312 TGGTAATGTAGTTTCAACATTACTTGCAGTTTCCAGTTAGTAAATAATAATTAAGCCCTAG 371
Db 1846 GAGATATATATATTAATAATTTGTTTGGTATTTTAAAGTAGTTAATTTTATTTATTTT 1905
Qy 372 TAAGTATAATTTAATTTATGTCATAAATTTGGAATAATCCATGGTACTTAAATTTT 431
Db 1906 TTTAATAGTATTTAAATGTTGTTTATATGTTGTTATTTTATTTTATTTTATTAATA 1965
Qy 432 ACCAAATTCATCGAACAACAAGTTGGCTATTTTGGATTGATATTTTGAATACT 491
Db 1966 GTTATATATATTTTATAAGATTGAAAGATTTTTCGATCTAGCAATTTATGTTAGT 2025
Qy 492 AGTACAGGAATATCATGTTGTAGTTGAATTTTTCAGTTAGAAACAATAATGAGTTAGAT 551
Db 2026 TTTAGAGAAATTTTGAATTTTATGAAAGTTTATTTAGAAATATATGTTGAAGTGAATA 2085
Qy 552 AGCTAAAGTATAATTTATTTGTAATTTAATAATGATGATGAGTTAGGCTATGATAATTA 611
Db 2086 TATTTTATTTTAAATAATTTATTTATTTTATTTTATTTTATTTTATTTTATTTT 2145
Qy 612 GTGAAACACCCCAAGAATGTTTATPACTTTTAAATTT 648
Db 2146 ATAGATTTTGAAGAGTTTATTTTATTTTATTTT 2182

RESULT 10

US-10-221-714A-27
; Sequence 27, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 27
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-27

Query Match 15.2%; Score 106.6; DB 8; Length 8666;
Best Local Similarity 49.0%; Pred. No. 1.9e-09;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

Qy 12 AAAGTTTTTTTTTTTGTATGATTTTAAATAAAATCATTTTCTTTTTTATTTATTTAT 71
Db 1547 AAAGTTTTTTTATTTATTTAATTTATTTATTAATAATTTTAAATTTTATTTATTTA 1606
Qy 72 ACTTTTAAGTTTATAGGTTACATGCAAGTGTCAGGTTAGTTTACATATATATACATGT 131
Db 1607 TATTTTAAGTTTATAGATATATGTTAATATGTTAGGTTTGTATATATATATATATGT 1666
Qy 132 GCCATGCTGTGTGCTGCCACCCATTAACCTACATGAAGTTTTTTTTAAATTTTATGTGACA 191
Db 1667 GTTATGTTGGTGTGTTGTTATTTAATTTA - TTATTTAGTATTAGGTATATTTTAAAT 1725
Qy 192 GTTTTAGTCATTTTCCCTAAATGAAAGTATCATAGTAAATCCATAAATTTGAAAAAATGT 251
Db 1726 GTTATTTTATTTTATTTTATTAAGATTTTATTAAGATTTATTAATGATTAATTTTATTTT 1785
Qy 252 TAACCTACTCTGATAAAAAAGTTTATAGTTTTCCTACTTTTAAAGCAAAATTCCTATAGGGCA 311
Db 1786 AGAGTAAATGGTTTATTTAAGGATGTTATAATTTTTCAGTTTATTTAGAGTTTATTTGTAAGATAT 1845
Qy 312 TGGTAATGTAGTTTCAACATTACTTGCAGTTTTCAGTTAGTAAATAATAATTAAGCCCTAG 371
Db 1846 GAGATATATATATTTAAATTTGTTTGGTATTTTAAAGTAGTTAATTTTATTTATTTT 1905
Qy 372 TAAGTATAATTTAATATTTGTCATAAATTTGGAATAATCCATGGTACTTAAATTTT 431
Db 1906 TTTAATAATGATTTAATAATGTTGTTTATATGTTGTTATTTTATTTTATTTTATTTAATA 1965
Qy 432 ACCAAATTTCCATGGAACAACAAGTTGGCTATTTTGGATTGATATTTTGAATACT 491
Db 1966 GTTATATATATTTTATAAGAGTTGAAAGAGTTTTCGATCTAGCAATTTATGTTAGT 2025
Qy 492 AGTACAGGAATATCATTTGTTAGTTGAATTTTTCAGCTTAGAAACAATAATGAGTTAGAT 551
Db 2026 TTTAGAGAAATTTTGAATTTTATTTGAAGTTTATTTAGAAATATATGTTGAAGTGAATA 2085
Qy 552 AGCTAAAGTATAATTTATTTGTAATTTAATAATGATGATGAGTTAGGCTATGATAATTA 611
Db 2086 TATTTTATTTTAAATAATTTATTTATTTTATTTTATTTTATTTTATTTTATTTT 2145
Qy 612 GTGAAACACCCCAAGAATGTTTATPACTTTTAAATTT 648
Db 2146 ATAGATTTTGAAGAGTTTATTTTATTTTATTTT 2182

RESULT 11

US-10-311-507-95
; Sequence 95, Application US/10311507
; Publication No. US20040115630A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and nucleic acids for the analysis of astrocytomas
; FILE REFERENCE: 5013.1013
; CURRENT APPLICATION NUMBER: US/10/311,507
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07538
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 95
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-507-95

Query Match 15.2%; Score 106.6; DB 8; Length 8666;

[illegible]

```

RESULT 12
US-10-433-793-207
; Sequence 207, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 207
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-207

```

```

RESULT 13
US-09-925-065A-477191/c
; Sequence 477191, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477191
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-477191
Query Match 15.1%; Score 105.8; DB 4; Length 493;

```



```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235941
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235941
```

```
Query Match          15.1%; Score 105.4; DB 6; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;

Qy 3 GTTTCACATAAAGTTTTTTTTTTTGGTACATGTTTAAATAAATATCATTTCTTTTTTAT 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGAGACATTTCTTTTTTTTCAATTTTAAGCATTTTAAATTTCTTTTAAAA 343

Qy 63 TATTATTATCT-----TTTAAGTTTTAGGTGACATGTGCAAAAGTGCAGGTTAGTTAC 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATTATCTTTTAAAGTTTTAGGTGACATGTGCAAAATGTGCAGGTTAGTTAC 283

Qy 118 ATATATATACATGTCCTGCTGCTGCACCCATTAACCTACATGCAAGTTTATTTT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGTCATGCTGATGCTGTCACCCATTAACCTATTTASCATTAGGTAT 223

Qy 178 AAAATTTTAGTGACAGTTTATGTC 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCCTAATGCTATCCCTACYC 200
```

```
RESULT 25
US-10-027-632-235942/c
; Sequence 235942, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235942
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235942

Query Match          15.1%; Score 105.4; DB 6; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;

Qy 3 GTTTCACATAAAGTTTTTTTTTTTGGTACATGTTTAAATAAATATCATTTCTTTTTTAT 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGAGACATTTCTTTTTTTTCAATTTTAAGCATTTTAAATTTCTTTTAAAA 343

Qy 63 TATTATTATCT-----TTTAAGTTTTAGGTGACATGTGCAAAAGTGCAGGTTAGTTAC 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATTATCTTTTAAAGTTTTAGGTGACATGTGCAAAATGTGCAGGTTAGTTAC 283

Qy 118 ATATATATACATGTCCTGCTGCTGCACCCATTAACCTACATGCAAGTTTATTTT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGTCATGCTGATGCTGTCACCCATTAACCTATTTASCATTAGGTAT 223

Qy 178 AAAATTTTAGTGACAGTTTATGTC 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCCTAATGCTATCCCTACYC 200
```

```
RESULT 26
US-10-027-632-235943/c
; Sequence 235943, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235943
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235943
```

```
Query Match          15.1%; Score 105.4; DB 6; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;

Qy 3 GTTTCACATAAAGTTTTTTTTTTTGGTACATGTTTAAATAAATATCATTTCTTTTTTAT 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGAGACATTTCTTTTTTTTCAATTTTAAGCATTTTAAATTTCTTTTAAAA 343

Qy 63 TATTATTATCT-----TTTAAGTTTTAGGTGACATGTGCAAAAGTGCAGGTTAGTTAC 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATTATCTTTTAAAGTTTTAGGTGACATGTGCAAAATGTGCAGGTTAGTTAC 283
```

QY 118 ATATATATACATGCGCATGCTGGTGTGCGACCCCACTTAACATCAATGAGTATTTT 177
Db 282 ATATGTATACATGTCATGCTGCTGCGACCCCACTTAACATCAATGAGTAT 223
QY 178 AAATTTTAGTGACAGTTTATGTC 200
Db 222 ATCTCCTAATGCTATCCCTACYC 200

RESULT 27
US-10-027-632-235941/c
; Sequence 235941, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235941
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235941

Query Match 15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;
QY 3 GTTTCACATAAAGTTTTTTTTTTCATGATGATTTTAAATAAATATCAATTTCTTTTAT 62
Db 402 GTTGAAGAGACATTTCTTTTTTTTTCATTTAAGCATTTTAAATTTCTTTTAAAA 343
QY 63 TATTATTACT-----TTTAAGTTTAGGTACATGCAAGTGTGAGGTAGTTAC 117
Db 342 TTTTATTATTATATCTTTAAAGTTTAAAGTTTAAAGTTGACATGTGCACATGTGAGGTAGTTAC 283
QY 118 ATATATATACATGCGCATGCTGGTGTGCGACCCCACTTAACATCAATGAGTATTTT 177
Db 282 ATATGTATACATGTCATGCTGCTGCGACCCCACTTAACATCAATGAGTATTT 223
QY 178 AAATTTTAGTGACAGTTTATGTC 200
Db 222 ATCTCCTAATGCTATCCCTACYC 200

RESULT 28
US-10-027-632-235942/c
; Sequence 235942, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235942
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235942

Query Match 15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;
QY 3 GTTTCACATAAAGTTTTTTTTTTCATGATGATTTTAAATAAATATCAATTTCTTTTAT 62
Db 402 GTTGAAGAGACATTTCTTTTTTTTTCATTTAAGCATTTTAAATTTCTTTTAAAA 343
QY 63 TATTATTACT-----TTTAAGTTTAGGTACATGCAAGTGTGAGGTAGTTAC 117
Db 342 TTTTATTATTATATCTTTAAAGTTTAAAGTTTAAAGTTGACATGTGCACATGTGAGGTAGTTAC 283
QY 118 ATATATATACATGCGCATGCTGGTGTGCGACCCCACTTAACATCAATGAGTATTTT 177
Db 282 ATATGTATACATGTCATGCTGCTGCGACCCCACTTAACATCAATGAGTATTT 223
QY 178 AAATTTTAGTGACAGTTTATGTC 200
Db 222 ATCTCCTAATGCTATCCCTACYC 200

RESULT 29
US-10-027-632-235943/c
; Sequence 235943, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235943

```

; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235943

Query Match      15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;

QY 3 GTTTCACATAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTAT 62
Db 402 GTTGAAGACATTTCTTTTTTTTTCATTTTAAGCATTTTAAATTTCTTTTAA 343
QY 63 TATTATTATAC-----TTTAAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTAC 117
Db 342 TTTTATTATTATACTTTAAAGTTTGGGTACATGTGCACATGTGCAGTTAGTTAC 283
QY 118 ATATATATACATGTGCCATGTGGTGTGTCGCCATTAACATCAATCAATTTT 177
Db 282 ATATGTATACATGTGTCATGTGCTGTGTCGCCATTAACATCAATTTAGGTAT 223
QY 178 AAATTTTGTACATTTTGTGTC 200
Db 222 ATCTCCTAATGCTATCCCTACYC 200

RESULT 30
US-09-818-657-3/c
; Sequence 3, Application US/09818657
; Publication No. US2003007773A1
; GENERAL INFORMATION:
; APPLICANT: BRANDON, Rhonda et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001006-CIP
; CURRENT APPLICATION NUMBER: US/09/818,657
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 2001-03-28
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 82938
; TYPE: DNA
; ORGANISM: Human
US-09-818-657-3

Query Match      15.1%; Score 105.4; DB 3; Length 82938;
Best Local Similarity 82.3%; Pred. No. 6.6e-09;
Matches 121; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGTATGATTTTAAATAAATATCATTTCTTTTATTTATTTATATACCT 75
Db 63261 TCCTTTGTTTATGTGGAACAAATTTGTTTATTTTATTTTATTTATTTATACCT 63202
QY 76 TTAAGTTTGGGTACATGTGCAAGTGTGAGTTAGTTACATATATATACATGTGCCA 135
Db 63201 TTCAGTTTGGGTACATGTGCAATGTGCAAGTGTGAGTTAGTTACATATGTATACATGTGCCA 63142
QY 136 TGCTGGTGTGCTGCACCCATTAACCTCA 162
Db 63141 TGCTGGTGTGCTGCACCCATTAACCTCA 63115

RESULT 31
US-11-136-623-3/c
; Sequence 3, Application US/11136623
; Publication No. US20050221437A1
; GENERAL INFORMATION:
; APPLICANT: BRANDON, Rhonda, et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001006-CIP
; CURRENT APPLICATION NUMBER: US/11/136,623
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 09/730,002
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 82938
; TYPE: DNA
; ORGANISM: Human
US-11-136-623-3

Query Match      15.1%; Score 105.4; DB 13; Length 82938;
Best Local Similarity 82.3%; Pred. No. 6.6e-09;
Matches 121; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGTATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTATACCT 75
Db 63261 TCCTTTGTTTATGTGGAACAAATTTGTTTATTTTATTTTATTTTATTTATTTATACCT 63202
QY 76 TTAAGTTTGGGTACATGTGCAAGTGTGAGTTAGTTACATATATATACATGTGCCA 135
Db 63201 TTCAGTTTGGGTACATGTGCAATGTGCAAGTGTGAGTTAGTTACATATGTATACATGTGCCA 63142
QY 136 TGCTGGTGTGCTGCACCCATTAACCTCA 162
Db 63141 TGCTGGTGTGCTGCACCCATTAACCTCA 63115

RESULT 32
US-10-301-480-578850
; Sequence 578850, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 578850
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
; LOCATION: 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167,
; LOCATION: 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
; LOCATION: 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
; LOCATION: 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
; LOCATION: 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226,
; LOCATION: 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 238, 239, 240, 241, 242, 243
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-578850

Query Match      15.0%; Score 105.2; DB 12; Length 989;

```

```
Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTTCACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTCTTTTTTTATT 63
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
441 TGTTCGAAGCATTTATTTATTTATTTTATTTTGGCGTATTTATTTATTTATTTATT 500

QY 64 ATTATTATACATTTTAAGTTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATAT 123
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
501 ATTACAGTACTTTTAAGTTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATATGT 560

QY 124 ATACATGTGCATGCTGCTGCTGCTGCAACCATTAACTC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
561 ATACATGTGCCATGCTGGTGGCTGCGCTGCACCACTAACTC 598

RESULT 33
US-10-301-480-1192259
; Sequence 1192259, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1192259
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
; LOCATION: 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167,
; LOCATION: 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
; LOCATION: 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
; LOCATION: 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
; LOCATION: 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226,
; LOCATION: 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 238, 239, 240, 241, 242, 243
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1192259

Query Match 15.0%; Score 105.2; DB 12; Length 989;
Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTTCACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTCTTTTTTTATT 63
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
441 TGTTCGAAGCATTTATTTATTTATTTTATTTTGGCGTATTTATTTATTTATTTATT 500

QY 64 ATTATTATACATTTTAAGTTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATAT 123
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
501 ATTACAGTACTTTTAAGTTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATATGT 560

QY 124 ATACATGTGCCATGCTGCTGCTGCTGCAACCATTAACTC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
561 ATACATGTGCCATGCTGGTGGCTGCGCTGCACCACTAACTC 598
```

```
RESULT 34
US-11-121-086-51
; Sequence 51, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 176760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-51

Query Match 15.0%; Score 104.8; DB 15; Length 176760;
Best Local Similarity 87.5%; Pred. No. 1.1e-08;
Matches 126; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 17 TTTTCTTTTGTGATGATTTTAAATAAAATATCATTTCTTTTTTATTTATTTACTTTT 76
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20705 TTTTATTTTAAATTTTATTTTAAATTTCTTTTTTATTTATTTATTTATTTATTT 20763

QY 77 TAAATTTTAGGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATACATGTGCCAT 136
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20764 TAAATTTTAGGGTACATGTGCATAATGTGCAGGTAGTTACATATGTACATGTGCCAT 20823

QY 137 GCTGGTGTCTGCCACCACTAACT 160
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20824 GCTGGTGTCTGCCACCACTAACT 20847

RESULT 35
US-10-322-281-214
; Sequence 214, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 72678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-214

Query Match 14.9%; Score 104.6; DB 8; Length 72678;
Best Local Similarity 80.8%; Pred. No. 8.9e-09;
Matches 122; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTCTTTTTTATTTATTTA 70
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68541 TACAGAACTCTTTTTTTTTTTTTTTTCTCTCTCTATATATTTTATTTATTTATTTA 68600

QY 71 TACTTTTAAAGTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATACATG 130
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68601 TACTTTTAAAGTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATATGTACATG 68660

QY 131 TGCCATGCTGGTGTGCTGCACCCCACTAACTC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68661 TGCCATGCTGGTGTGCTGCACCCCACTAACTC 68691
```

RESULT 36

US-10-756-149-321
; Sequence 321, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziiz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 321
; LENGTH: 146882
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-321

Query Match 14.9%; Score 104.6; DB 10; Length 126882;
Best Local Similarity 80.8; Pred. No. 1.1e-08;
Matches 122; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 11 TAAAGTGTCTTTTTCATGATTATAAAAAATATCATTTCTCTCTATATATTTTATTATTATTA 70
DB 89734 TACAGAACTCTTTTTTTTTTTTTTTTTCATTTCTCTCTATATATTTTATTATTATTA 89793

QY 71 TACTTTTAAGTTTTAGGGTCAATGTGCAGAGTGCGAGGTAGTTACATATATATACATG 130
DB 89794 TACTTTTAAAGTTTTAGGGTCAATGTGCAGAGTTAGTTACATATATATACATG 89853

QY 131 TGCCATCTCGTGTGCTGCCACCATTAACTC 161
DB 89854 TGCCATCTCGTGTGCTGCCACCCTAACCTC 89884

RESULT 37

US-10-719-993-6940
; Sequence 6940, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6940
; LENGTH: 1790242
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1790242)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10)
US-10-719-993-6940

Query Match 14.9%; Score 104.6; DB 9; Length 1790242;
Best Local Similarity 89.2; Pred. No. 2.5e-08;
Matches 124; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 24 TTTTTGATGATTTTAAATAAAAATATCATTTCTTTTTTTTATTATTATTATATCTTTTAAAGTTT 83
DB 586253 TGTTTCATCATTTTATTATTATTTTATTTTATTTTATTATTATTATTATATAC-TTTAAAGTTT 586311

QY 84 TAGGGTACATGTGCAGAGTGTGCAGGTAGTTACATATATATATACATGTGCCATGCTGGTG 143
DB 586312 TAGGGTACATGTGCACATGTGCAGGTAGTTACATATGTATATCATGTGCATGCTGGTG 586371

[illegible]

```

1  RESULT 40
2  US-99-984-429-469/c
3  ; Sequence 469, Application US/09984429
4  ; Publication No. US2004001032A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Rosen et al.
7  ; TITLE OF INVENTION: 53 Human Secreted Proteins
8  ; FILE REFERENCE: PZ018P2
9  ; CURRENT APPLICATION NUMBER: US/09/984,429
10 ; CURRENT FILING DATE: 2001-10-30
11 ; PRIOR APPLICATION NUMBER: 60/244,591
12 ; PRIOR FILING DATE: 2000-11-01
13 ; PRIOR APPLICATION NUMBER: 09/288,143
14 ; PRIOR FILING DATE: 1999-04-08
15 ; PRIOR APPLICATION NUMBER: PCT/US98/21142
16 ; PRIOR FILING DATE: 1998-10-08
17 ; PRIOR APPLICATION NUMBER: 60/061,463
18 ; PRIOR FILING DATE: 1997-10-09
19 ; PRIOR APPLICATION NUMBER: 60/061,529
20 ; PRIOR FILING DATE: 1997-10-09
21 ; PRIOR APPLICATION NUMBER: 60/071,498
22 ; PRIOR FILING DATE: 1997-10-09
23 ; PRIOR APPLICATION NUMBER: 60/061,527
24 ; PRIOR FILING DATE: 1997-10-09
25 ; PRIOR APPLICATION NUMBER: 60/061,536
26 ; PRIOR FILING DATE: 1997-10-09
27 ; PRIOR APPLICATION NUMBER: 60/061,532
28 ; PRIOR FILING DATE: 1997-10-09
29 ; NUMBER OF SEQ ID NOS: 727
30 ; SOFTWARE: Patentin Ver. 2.0
31 ; SEQ ID NO 469
32 ; LENGTH: 42595
33 ; TYPE: DNA
34 ; ORGANISM: Homo sapiens
35 ; FEATURE:
36 ; NAME/KEY: misc.feature
37 ; LOCATION: (7234)..(7234)
38 ; OTHER INFORMATION: n equals a,t,g, or c
39 ;
40 ;
41 ;
42 ;
43 ;
44 ;
45 ;
46 ;
47 ;
48 ;
49 ;
50 ;
51 ;
52 ;
53 ;
54 ;
55 ;
56 ;
57 ;
58 ;
59 ;
60 ;
61 ;
62 ;
63 ;
64 ;
65 ;
66 ;
67 ;
68 ;
69 ;
70 ;
71 ;
72 ;
73 ;
74 ;
75 ;
76 ;
77 ;
78 ;
79 ;
80 ;
81 ;
82 ;
83 ;
84 ;
85 ;
86 ;
87 ;
88 ;
89 ;
90 ;
91 ;
92 ;
93 ;
94 ;
95 ;
96 ;
97 ;
98 ;
99 ;
100 ;
101 ;
102 ;
103 ;
104 ;
105 ;
106 ;
107 ;
108 ;
109 ;
110 ;
111 ;
112 ;
113 ;
114 ;
115 ;
116 ;
117 ;
118 ;
119 ;
120 ;
121 ;
122 ;
123 ;
124 ;
125 ;
126 ;
127 ;
128 ;
129 ;
130 ;
131 ;
132 ;
133 ;
134 ;
135 ;
136 ;
137 ;
138 ;
139 ;
140 ;
141 ;
142 ;
143 ;
144 ;
145 ;
146 ;
147 ;
148 ;
149 ;
150 ;
151 ;
152 ;
153 ;
154 ;
155 ;
156 ;
157 ;
158 ;
159 ;
160 ;
161 ;
162 ;
163 ;
164 ;
165 ;
166 ;
167 ;
168 ;
169 ;
170 ;
171 ;
172 ;
173 ;
174 ;
175 ;
176 ;
177 ;
178 ;
179 ;
180 ;
181 ;
182 ;
183 ;
184 ;
185 ;
186 ;
187 ;
188 ;
189 ;
190 ;
191 ;
192 ;
193 ;
194 ;
195 ;
196 ;
197 ;
198 ;
199 ;
200 ;
201 ;
202 ;
203 ;
204 ;
205 ;
206 ;
207 ;
208 ;
209 ;
210 ;
211 ;
212 ;
213 ;
214 ;
215 ;
216 ;
217 ;
218 ;
219 ;
220 ;
221 ;
222 ;
223 ;
224 ;
225 ;
226 ;
227 ;
228 ;
229 ;
230 ;
231 ;
232 ;
233 ;
234 ;
235 ;
236 ;
237 ;
238 ;
239 ;
240 ;
241 ;
242 ;
243 ;
244 ;
245 ;
246 ;
247 ;
248 ;
249 ;
250 ;
251 ;
252 ;
253 ;
254 ;
255 ;
256 ;
257 ;
258 ;
259 ;
260 ;
261 ;
262 ;
263 ;
264 ;
265 ;
266 ;
267 ;
268 ;
269 ;
270 ;
271 ;
272 ;
273 ;
274 ;
275 ;
276 ;
277 ;
278 ;
279 ;
280 ;
281 ;
282 ;
283 ;
284 ;
285 ;
286 ;
287 ;
288 ;
289 ;
290 ;
291 ;
292 ;
293 ;
294 ;
295 ;
296 ;
297 ;
298 ;
299 ;
300 ;
301 ;
302 ;
303 ;
304 ;
305 ;
306 ;
307 ;
308 ;
309 ;
310 ;
311 ;
312 ;
313 ;
314 ;
315 ;
316 ;
317 ;
318 ;
319 ;
320 ;
321 ;
322 ;
323 ;
324 ;
325 ;
326 ;
327 ;
328 ;
329 ;
330 ;
331 ;
332 ;
333 ;
334 ;
335 ;
336 ;
337 ;
338 ;
339 ;
340 ;
341 ;
342 ;
343 ;
344 ;
345 ;
346 ;
347 ;
348 ;
349 ;
350 ;
351 ;
352 ;
353 ;
354 ;
355 ;
356 ;
357 ;
358 ;
359 ;
360 ;
361 ;
362 ;
363 ;
364 ;
365 ;
366 ;
367 ;
368 ;
369 ;
370 ;
371 ;
372 ;
373 ;
374 ;
375 ;
376 ;
377 ;
378 ;
379 ;
380 ;
381 ;
382 ;
383 ;
384 ;
385 ;
386 ;
387 ;
388 ;
389 ;
390 ;
391 ;
392 ;
393 ;
394 ;
395 ;
396 ;
397 ;
398 ;
399 ;
400 ;
401 ;
402 ;
403 ;
404 ;
405 ;
406 ;
407 ;
408 ;
409 ;
410 ;
411 ;
412 ;
413 ;
414 ;
415 ;
416 ;
417 ;
418 ;
419 ;
420 ;
421 ;
422 ;
423 ;
424 ;
425 ;
426 ;
427 ;
428 ;
429 ;
430 ;
431 ;
432 ;
433 ;
434 ;
435 ;
436 ;
437 ;
438 ;
439 ;
440 ;
441 ;
442 ;
443 ;
444 ;
445 ;
446 ;
447 ;
448 ;
449 ;
450 ;
451 ;
452 ;
453 ;
454 ;
455 ;
456 ;
457 ;
458 ;
459 ;
460 ;
461 ;
462 ;
463 ;
464 ;
465 ;
466 ;
467 ;
468 ;
469 ;
470 ;
471 ;
472 ;
473 ;
474 ;
475 ;
476 ;
477 ;
478 ;
479 ;
480 ;
481 ;
482 ;
483 ;
484 ;
485 ;
486 ;
487 ;
488 ;
489 ;
490 ;
491 ;
492 ;
493 ;
494 ;
495 ;
496 ;
497 ;
498 ;
499 ;
500 ;
501 ;
502 ;
503 ;
504 ;
505 ;
506 ;
507 ;
508 ;
509 ;
510 ;
511 ;
512 ;
513 ;
514 ;
515 ;
516 ;
517 ;
518 ;
519 ;
520 ;
521 ;
522 ;
523 ;
524 ;
525 ;
526 ;
527 ;
528 ;
529 ;
530 ;
531 ;
532 ;
533 ;
534 ;
535 ;
536 ;
537 ;
538 ;
539 ;
540 ;
541 ;
542 ;
543 ;
544 ;
545 ;
546 ;
547 ;
548 ;
549 ;
550 ;
551 ;
552 ;
553 ;
554 ;
555 ;
556 ;
557 ;
558 ;
559 ;
560 ;
561 ;
562 ;
563 ;
564 ;
565 ;
566 ;
567 ;
568 ;
569 ;
570 ;
571 ;
572 ;
573 ;
574 ;
575 ;
576 ;
577 ;
578 ;
579 ;
580 ;
581 ;
582 ;
583 ;
584 ;
585 ;
586 ;
587 ;
588 ;
589 ;
590 ;
591 ;
592 ;
593 ;
594 ;
595 ;
596 ;
597 ;
598 ;
599 ;
600 ;
601 ;
602 ;
603 ;
604 ;
605 ;
606 ;
607 ;
608 ;
609 ;
610 ;
611 ;
612 ;
613 ;
614 ;
615 ;
616 ;
617 ;
618 ;
619 ;
620 ;
621 ;
622 ;
623 ;
624 ;
625 ;
626 ;
627 ;
628 ;
629 ;
630 ;
631 ;
632 ;
633 ;
634 ;
635 ;
636 ;
637 ;
638 ;
639 ;
640 ;
641 ;
642 ;
643 ;
644 ;
645 ;
646 ;
647 ;
648 ;
649 ;
650 ;
651 ;
652 ;
653 ;
654 ;
655 ;
656 ;
657 ;
658 ;
659 ;
660 ;
661 ;
662 ;
663 ;
664 ;
665 ;
666 ;
667 ;
668 ;
669 ;
670 ;
671 ;
672 ;
673 ;
674 ;
675 ;
676 ;
677 ;
678 ;
679 ;
680 ;
681 ;
682 ;
683 ;
684 ;
685 ;
686 ;
687 ;
688 ;
689 ;
690 ;
691 ;
692 ;
693 ;
694 ;
695 ;
696 ;
697 ;
698 ;
699 ;
700 ;
701 ;
702 ;
703 ;
704 ;
705 ;
706 ;
707 ;
708 ;
709 ;
710 ;
711 ;
712 ;
713 ;
714 ;
715 ;
716 ;
717 ;
718 ;
719 ;
720 ;
721 ;
722 ;
723 ;
724 ;
725 ;
726 ;
727 ;
728 ;
729 ;
730 ;
731 ;
732 ;
733 ;
734 ;
735 ;
736 ;
737 ;
738 ;
739 ;
74
```

Query Match	14.9%	Score 104.2	DB 3	Length 42595
Best Local Similarity	86.9%	Pred. No. 8.e-09		
Matches 126	Conservative 0	Mismatches 18	Indels 1	Gaps 1
Qy	17	TTTCTTTTCTTGATGATTTAATAAATAATCACTTTCTTTTTTTTATTATTATTATTACTTT	76	
Db	1952	TCCTTTTTTAAATTTAAATTTAAATTTTATTATTATTATTATTATTATTATTATTAC-TT	18894	
Qy	77	TAAGTTTTCAGGTACATGTGCAAAAGTGTGCAGGTTAGTTTACATATATATACATGTGCCAT	136	
Db	18893	TAAGTTTTCAGGTACATGTGCACATTTGCGAGGTTAGTTTACATATCTATACATGTGCCAT	18834	
Qy	137	GCTGGGTGTGTCGACCACTTAATCTC	161	
Db	18833	GCTGGGTGTGTCGACCACTTAATCTC	18809	

RESULT 41
US-10-087-192-238/c
: Sequence 238. Application US/10087192

```

; Publication No. US20020182586A1
; GENERAL INFORMATION: David W.
; APPLICANT: Morris, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 127369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(127369)
; OTHER INFORMATION: n = A,T,C or G
; US-10-087-192-238

Query Match          14.9%; Score 104; DB 6; Length 127369;
Best Local Similarity 95.5%; Pred. No. 1.4e-08;
Matches 107; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      50  TTTCCTTTTATTATTATTATATATATCTTTTAACTTTTAGGTACATGTGCANAAGTGTGCAGG 109
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      114373 TTTTATTATTATTATTATTATATCTTTTAACTTTTAGGTACATGTGCACAATGTCAGG 114314

Qy      110  TTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      114313 TTAGTTACATATGTATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 114262

RESULT 42
US-11-121-086-98
; Sequence 98, Application US/11121086
; Publication No. US20050266459A1

```

```

; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 171732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-98

Query Match          14.9%; Score 104; DB 15; Length 171732;
Best Local Similarity 83.3%; Pred. No. 1.5e-08;
Matches 130; Conservative 0; Mismatches 25; Indels 1; Gaps

Qy      6 TCACATAAGTTTTTTTTTTTGGATGATTTTATAAATAATCATTTCTTTTTTTTATTA
Db      38959 TCTATTTTTATTTATTTTATTTTATTTTATTTTAAATTTCTTATTTTATTA
Qy      66 TATTATACTTTTAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATA
Db      39019 TATTATAC-TTTTAAAGTTTTAGGGTACATGTGCATAAATGTGCAGGTTAGTTACATATGTA
Qy      126 ACATGTGCATGCTGGTGTGCTGCACCCATTAACTC 161

```


Db 39078 ACATGTGCCATGCTGCTGTGCTGCACCCATTAACTC 39113

RESULT 43

US-10-517-905-19/c
; Sequence 19, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetrii, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 19
; LENGTH: 191150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(49)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (50)..(2330)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2331)..(2648)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (2649)..(4902)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (4903)..(5163)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (5164)..(6154)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (6155)..(6285)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (6286)..(8524)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (8525)..(8696)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (8697)..(8787)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (8788)..(8977)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (8978)..(166510)
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (10577)..(10676)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10577)..(10676)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (14335)..(14434)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14335)..(14434)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (16247)..(16346)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16247)..(16346)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17457)..(17457)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21818)..(21818)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36293)..(36298)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36314)..(36314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36316)..(36316)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36432)..(36433)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (36774)..(36873)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36774)..(36873)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59740)..(59740)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59740)..(59740)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59742)..(59742)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59742)..(59744)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59744)..(59744)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59749)..(59755)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature

```

1 / LOCATION: (59749)..(59755)
2 / OTHER INFORMATION: n is a, c, g, or t
3 / FEATURE:
4 / NAME/KEY: Unsure
5 / LOCATION: (59759)..(59760)
6 / OTHER INFORMATION: n = any nucleic acid
7 / FEATURE:
8 / NAME/KEY: misc_feature
9 / LOCATION: (59759)..(59760)
10 / OTHER INFORMATION: n is a, c, g, or t
11 / FEATURE:
12 / NAME/KEY: misc_feature
13 / LOCATION: (59765)..(59766)
14 / OTHER INFORMATION: n is a, c, g, or t
15 / FEATURE:
16 / NAME/KEY: Unsure
17 / LOCATION: (59776)..(59875)
18 / OTHER INFORMATION: n = any nucleic acid
19 / FEATURE:
20 / NAME/KEY: misc_feature
21 / LOCATION: (59776)..(59875)
22 / OTHER INFORMATION: n is a, c, g, or t
23 / FEATURE:
24 / NAME/KEY: Unsure
25 / LOCATION: (82745)..(82844)
26 / OTHER INFORMATION: n = any nucleic acid
27 / FEATURE:
28 / NAME/KEY: misc_feature
29 / LOCATION: (82745)..(82844)
30 / OTHER INFORMATION: n is a, c, g, or t
31 / FEATURE:
32 / NAME/KEY: Unsure
33 / LOCATION: (96508)..(96607)
34 / OTHER INFORMATION: n = any nucleic acid
35 / FEATURE:
36 / NAME/KEY: misc_feature
37 / LOCATION: (96508)..(96607)
38 / OTHER INFORMATION: n is a, c, g, or t
39 / FEATURE:
40 / NAME/KEY: Unsure
41 / LOCATION: (147675)..(147774)
42 / OTHER INFORMATION: n = any nucleic acid
43 / FEATURE:
44 / NAME/KEY: misc_feature
45 / LOCATION: (147675)..(147774)
46 / OTHER INFORMATION: n is a, c, g, or t
47 / FEATURE:
48 / NAME/KEY: Unsure
49 / LOCATION: (157152)..(157251)
50 / OTHER INFORMATION: n = any nucleic acid
51 / FEATURE:
52 / NAME/KEY: misc_feature
53 / LOCATION: (157152)..(157251)
54 / OTHER INFORMATION: n is a, c, g, or t
55 / FEATURE:
56 / NAME/KEY: misc_feature
57 / LOCATION: (161475)..(161574)
58 / OTHER INFORMATION: n is a, c, g, or t
59 / FEATURE:

```

Query Match	14.9%;	Score 104;	DB 12;	Length 191150;
Best Local Similarity	83.3%;	Pred. No. 1.6e-08;		
Matches 130;	Conservative 0;	Mismatches 25;	Indels 1;	Gaps 1;
QY	6	TCACATAAAGTTTTTTTTTTTCATGATTTTAAATAAATAATCATTTTTCTTTTTTTTATTTAT	65	
DB	35430	TCTTATTTTATTATTTTATTTTATTTTATTTTATTTTAAATTTTCTTATTTTATTTATTTATTTAT	35371	
QY	66	TATTATACTTTTTAAGTTTTTAGGTCACATGTCAAAGTGTGCAGGTTAGTTACATATATAT	125	
DB	35370	TATTATAC-TTTTAAGTTTTTAGGTCACATGTCATATGTCAGGTTAGTTACATATGTTAT	35312	
QY	126	ACATGTGCCATGCTGTGTGCTGCACCCATTAACTC	161	

Db
35311 ACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 35276

```

RESULT 44
US-10-087-192-1330/c
; Sequence 1330, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 1330
; LENGTH: 102980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1330

```

Query Match 14.8%; Score 103.8; DB 6; Length 102980;
Best Local Similarity 81.6%; Pred. No. 1.4e-08;
Matches 120; Conservative 0; Mismatches 27; Indels 0;

Qy	15	GTGTTTTTTTTTGATGATGATTTAAATAAATATCATTTCTCTTTTTTATATATATATATATACT	74
Db	84334	GCCTTTTATATTTATTTATTTTATTTTATATATATATATATATATTTTTTTTTTTTTTACT	84275
Qy	75	TTTAAAGTTTTAGGGTACATGTCGAAGTGTGCAGGTTAGTTACATATATATATACATGTGCC	134
Db	84274	TTTAAAGTTTTAGGGTACATGTCGACATGTGTGAGGTTAGTTACATATGTATACATGTGCC	84215
Qy	135	ATGCTGGTGTGCTGCACCCATAAAGTC	161
Db	84214	ATGCTGGTGCATGACACCCATAAAGTC	84188

```

RESULT 45
US-10-741-600-17645
; Sequence 17645, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17645
; LENGTH: 103660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Table
US-10-741-600-17645

```

Query Match 14.8%; Score 103.8; DB 9; Length 10360;
Best Local Similarity 87.4%; Pred. No. 1.4e-08;
Matches 125; Conservative 0; Mismatches 17; Indels 1; Gaps 1

Qy 19 TTTTTCCTTCGATGATTTTAAATAAATATCATCTTCCTTTTATATATATATATATCTTTTA 78

[illegible]

```

RESULT 46
US-10-995-561-13253
; Sequence 13253, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13253
; LENGTH: 103660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see
US-10-995-561-13253

```

	Query Match	14.8%	Score 103.8	DB 10	Length 103660
	Best Local Similarity	87.4%	Pred. No. 1.4e-08		
	Matches 125	Conservative 0	Mismatches 17	Indels 1	Gaps 1
QY	19	TTTTTTTTTTCATGATTTTAAATAATATCATTTCTCTTTTTTATTATTATTATATCTTTTA	78		
Db	52806	TTTTTTTTTTTTTTTTTGAAGTGGAGTTTCAGTCTCTTTTTTATTATTATTATATAC-TTTTA	52864		
QY	79	AGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGC	138		
Db	52865	AGTTTTAGGGTACATGTGCACATGTGCAGGTAGTTACATATGTATACATGTGCCATGC	52924		
QY	139	TGGTGTGCTGCACCCCATTTAACTC	161		
Db	52925	TGGTGTACCGCACCCCATTTAACTC	52947		

```

RESULT 47
US-10-301-480-577167
; Sequence 577167, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 577167
; LENGTH: 987
; TYPE: DNA

```

; ORGANISM: Homo sapien									
US-10-301-480-577167									
Query Match	14.8%;	Score	103.6;	DB	12;	Length	987;		
Best Local Similarity	78.5%;	Pred. No.	3.3e-09;						
Matches	124;	Conservative	0;	Mismatches	34;	Indels	0;	Gaps	0;
Qy	4	TTTCACATAAAGTTTTTTTTTTTTCATCATTTTATAAAATATCATTTTTCTTTTTTATT	63						
Db	635	TTCCAAATGATCTCTTTGTTTCTTGATGTTGTTCTTTTTTTTTCTTTTTTAT	694						
Qy	64	ATTATTATACTTTTAAAGTTTATGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATAT	123						
Db	695	TATTATTATACTTTTAAAGTTTTTATGGGTACATGTGCAAAATGTGCAGGTTAGTTACATATGT	754						
Qy	124	ATACATGTGCCATGCTGCTGTGCTGCACCCCAATTAAC TC	161						
Db	755	ATACATGTGCCATGCTGCTGTGCTGCACCCCAATTAAC TC	792						

```

RESULT 48
US-10-301-480-1190576
; Sequence 1190576, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1190576
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1190576

```

	Query Match	14.8%	Score 103.6	DB 12	Length 987
	Best Local Similarity	78.5%	Pred. No. 3.3e-09		
	Matches 124	Conservative 0	Mismatches 34	Indels 0	Gaps 0
Qy	4	TTTCACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTCTTTTTTTATT	63		
Db	635	TTCCAAATGATTCCTTTGTTTCTTGATGTTGTGTTCTTTTTTTTTTTTTTTAT	694		
Qy	64	ATTATTATACTTTTTAAAGTTTTTAGGGTACATGTGCAAAAGTGTGCAGTTAGTTACATATAT	123		
Db	695	TATTAATTACTTTAAAGTTTTTAGGGTACATGTGCACAATGTGCAGTTAGTTACATATCT	754		
Qy	124	ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC	161		
Db	755	ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC	792		

```

RESULT 49
US-09-949-654-3/c
; Sequence 3, Application US/09949654
; Patent No. US2002012764A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572

```


; Sequence 661, Application US/10074095
; Publication No. US20030077704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,212
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,207
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,245
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,244
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,217
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,211
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,215
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,264
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,214
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,297
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/232,400
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,081
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,080
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,414
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,244
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,064
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08

Query Match 14.7%; Score 103.2; DB 6; Length 24132;
Best Local Similarity 83.6%; Pred. No. 1.1e-08;
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 21 TTTTGTGATGATTTAAATAAATATCATTTTCTTTTATTTATTTATTTTAAAG 80
Db 19204 TTTATTTTAAATTTTAAACAATTTTCTTTTATTTTATTTTAAAG 19145

QY 81 TTTTAGGGTACATGCGAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140
Db 19144 TTTTAGGGTACATGCGAAATGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 19085

QY 141 GTGTGCTGCACCCCACTTAACT 160
Db 19084 GTGCGTGCACCCCACTTAACT 19065

RESULT 53

US-10-212-872-661/c
; Sequence 661, Application US/10212872
; Publication No. US20030215893A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C2
; CURRENT APPLICATION NUMBER: US/10/212,872
; CURRENT FILING DATE: 2002-08-07
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 661
; LENGTH: 24132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-872-661

Query Match 14.7%; Score 103.2; DB 7; Length 24132;
Best Local Similarity 83.6%; Pred. No. 1.1e-08;
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 21 TTTTGTGATGATTTAAATAAATATCATTTTCTTTTATTTATTTATTTTAAAG 80
Db 19204 TTTATTTTAAATTTTAAACAATTTTCTTTTATTTTATTTTAAAG 19145

QY 81 TTTTAGGGTACATGCGAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140
Db 19144 TTTTAGGGTACATGCGAAATGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 19085

QY 141 GTGTGCTGCACCCCACTTAACT 160
Db 19084 GTGCGTGCACCCCACTTAACT 19065

RESULT 54
US-10-330-773-76/c
; Sequence 76, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 118544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-773-76

Query Match 14.7%; Score 103.2; DB 11; Length 118544;
Best Local Similarity 83.6%; Pred. No. 1.9e-08;
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 21 TTTTGTGATGATTTAAATAAATATCATTTTCTTTTATTTATTTATTTTAAAG 80
Db 113985 TTTATTTTAAATTTTAAACAATTTTCTTTTATTTTATTTTAAAG 113926

QY 81 TTTTAGGGTACATGCGAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140
Db 113925 TTTTAGGGTACATGCGAAATGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 113866

QY 141 GTGTGCTGCACCCCACTTAACT 160
Db 113865 GTGCGTGCACCCCACTTAACT 113846

RESULT 55
US-10-301-480-570607

; Sequence 570607, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570607
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-570607

Query Match 14.7%; Score 103; DB 12; Length 865;
Best Local Similarity 85.7%; Pred. No. 4.1e-09;
Matches 126; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 15 GTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACT 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 GTTTTGTGTTTCATATTTAAATTTTAAATTTTATTTTATTTATTTATTTAC- 711
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 75 TTTAGTTTTAGGGTACATGTCGAAGTGTGCAGTTAGTTACATATATACATGTGCC 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 712 TTTAGTTTTAGGGTACATGTCGAATGTGCAGTTAGTTACATACGTATACATTTGCC 771
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 135 ATGCTGGTGTGCTGCACCACTAACTC 161
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 772 ATGCTGGTGTGCTGCACCACTAACTC 798
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 56

US-10-301-480-1184016
; Sequence 1184016, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1184016
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1184016

Query Match 14.7%; Score 103; DB 12; Length 865;
Best Local Similarity 85.7%; Pred. No. 4.1e-09;
Matches 126; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 15 GTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACT 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 GTTTTGTGTTTCATATTTAAATTTTAAATTTTATTTTATTTATTTATTTAC- 711
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 75 TTTAGTTTTAGGGTACATGTCGAAGTGTGCAGTTAGTTACATATATACATGTGCC 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 712 TTTAGTTTTAGGGTACATGTCGAATGTGCAGTTAGTTACATACGTATACATTTGCC 771
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 135 ATGCTGGTGTGCTGCACCACTAACTC 161
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 772 ATGCTGGTGTGCTGCACCACTAACTC 798
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 57

US-10-301-480-552761/c
; Sequence 552761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552761
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-552761

Query Match 14.7%; Score 103; DB 12; Length 987;
Best Local Similarity 82.5%; Pred. No. 4.2e-09;
Matches 118; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTTTAA 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 493 TTTATTTTATTTTGTGTATTTATTTATTTATTTATTTATTTATTTATTTAA 434
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 80 GTTTTAGGTACATGTCGAAGTGTGCAGTTAGTTACATATATACATGTGCCATGCT 139
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 433 GTTTTAGGTACATGTCGAATGTGCAGTTAGTTACATATGATATACATGTGCCATGCT 374
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 140 GGTGTGCTGCACCACTAACTCA 162
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 373 GGTGTGCTGCACCACTAACTCA 351
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 58

US-10-301-480-1166170/c
; Sequence 1166170, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1166170
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166170

Query Match 14.7%; Score 103; DB 12; Length 987;
Best Local Similarity 82.5%; Pred. No. 4.2e-09;
Matches 118; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTTTAA 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
QY 16 TTTTCTTTTGTGATGATTTTAATAAATATCACTTTCTTTTATTATTATTATATCTT 75
Db 260 TTTCACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTATTATT 201

QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCCATTAACTC 161
Db 140 TGTGGTGTGCTGCCACCCATTAACTC 115
```

RESULT 62

```
US-10-027-632-256998/c
; Sequence 256998, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256998
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256998
```

Query Match 14.7%; Score 102.8; DB 7; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
QY 16 TTTTCTTTTGTGATGATTTTAATAAATATCACTTTCTTTTATTATTATTATCTT 75
Db 260 TTTCACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTATTATT 201

QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCCATTAACTC 161
Db 140 TGTGGTGTGCTGCCACCCATTAACTC 115
```

RESULT 63

```
US-10-301-480-91798/c
; Sequence 91798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
```

```
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91798
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-91798
```

```
Query Match 14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAATAAATATCACTTTCTTTTATTATTATTATCTT 75
Db 260 TTTCACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTATTATT 201

QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCCATTAACTC 161
Db 140 TGTGGTGTGCTGCCACCCATTAACTC 115
```

RESULT 64

```
US-10-301-480-91799/c
; Sequence 91799, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91799
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-91799
```

Query Match 14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
QY 16 TTTTCTTTTGTGATGATTTTAATAAATATCACTTTCTTTTATTATTATTATCTT 75
Db 260 TTTCACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTATTATT 201

QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCCATTAACTC 161
Db 140 TGTGGTGTGCTGCCACCCATTAACTC 115
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 07:08:55 ; Search time 286 Seconds
(without alignments)
3516.007 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_A146311

Perfect score: 700

Sequence: 1 ctgtttcacataaagtgtttt.....gccttttagtgatggca 700

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 899801 seqs, 718270062 residues

Total number of hits satisfying chosen parameters: 1799602

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 70 summaries

Database : Published Applications NA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCF_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	110.8	15.8	1000	US-11-266-748A-196825	Sequence 196825,
C 2	106.6	15.2	8666	US-10-517-441-283	Sequence 283, App
C 3	106.6	15.2	8666	US-10-517-441-557	Sequence 557, App
C 4	104.6	14.9	72678	US-10-539-228-214	Sequence 214, App
C 5	103.4	14.8	70665	US-10-505-928-596	Sequence 596, App
C 6	101.6	14.5	1615	US-11-266-748A-58095	Sequence 58095, A
C 7	100.4	14.3	1577	US-11-266-748A-25751	Sequence 25751, A
C 8	99.8	14.3	1000	US-11-266-748A-197923	Sequence 197923, A
C 9	99.8	14.3	8666	US-10-517-441-19	Sequence 19, Appl
C 10	99.8	14.3	1237661	US-11-266-748A-29041	Sequence 29041, A
C 11	99.6	14.2	122568	US-11-266-748A-23292	Sequence 23292, A
C 12	99.2	14.2	1000	US-11-266-748A-205304	Sequence 205304, A
C 13	98.8	14.1	83965	US-10-539-228-826	Sequence 826, App
C 14	98.8	14.1	110096	US-11-266-748A-61303	Sequence 61303, A
C 15	97.8	14.0	1000	US-11-266-748A-207140	Sequence 207140, A
C 16	97.8	14.0	301477	US-10-539-228-456	Sequence 456, App
C 17	97.4	13.9	52987	US-10-539-228-386	Sequence 386, App
C 18	97.2	13.9	638	US-11-266-748A-209478	Sequence 209478, A
C 19	97.2	13.9	301477	US-10-539-228-456	Sequence 456, App
C 20	97	13.9	131546	US-11-266-748A-60109	Sequence 60109, A
C 21	96.8	13.8	1000	US-11-266-748A-290116	Sequence 290116, A
C 22	96.8	13.8	1000	US-11-266-748A-341545	Sequence 341545, A
C 23	96.8	13.8	261789	US-11-260-842-1	Sequence 1, Appl
C 24	96.8	13.8	421987	US-11-266-748A-28210	Sequence 28210, A

ALIGNMENTS

RESULT 1

US-11-266-748A-196825/c
; Sequence 196825, Application US/11266748A
; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and
; Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; PRIOR FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

Sequence 117289,
Sequence 159453,
Sequence 288898,
Sequence 340327,
Sequence 399825,
Sequence 470871,
Sequence 3, Appl
Sequence 232, Appl
Sequence 29045, A
Sequence 25123, A
Sequence 204505,
Sequence 60044, A
Sequence 220785,
Sequence 284468,
Sequence 335897,
Sequence 394477,
Sequence 465523,
Sequence 75, Appl
Sequence 25150, A
Sequence 60108, A
Sequence 219620,
Sequence 239532,
Sequence 25123, A
Sequence 86, Appl
Sequence 87, Appl
Sequence 28223, A
Sequence 79, Appl
Sequence 29045, A
Sequence 23277, A
Sequence 60144, A
Sequence 50139, A
Sequence 202832,
Sequence 23474, A
Sequence 23170, A
Sequence 29041, A
Sequence 200176,
Sequence 60803, A
Sequence 29039, A
Sequence 211402,
Sequence 37, Appl
Sequence 59086, A
Sequence 22833, A
Sequence 200842,
Sequence 25022, A
Sequence 23809, A
Sequence 60803, A

```
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 196825
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-196825

Query Match      15.8%; Score 110.8; DB 8; Length 1000;
Best Local Similarity 84.9%; Pred. No. 4.9e-11;
Matches 124; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAAAATATCATTTCTTTTATTATTATTATACCTT 75
DB 615 TTAATTTTATTTTATTTTATTTTATTTTCTATTTTATTATTATTATTATTTACTT 556

QY 76 TTAAGTTTATAGGTACATGTGCAAGGTGTCAGGTAGTTACATATATATACATGTGCCA 135
DB 555 TTAAGTTTATAGGTACATGTGCAATGTGCAAGGTAGTTACATATATATACATGTGCCA 496

QY 136 TCGTGGTGTCTGCACCATTAATCT 161
DB 495 TCGTGGTGTCTGCACCATTAATCT 470

RESULT 2
US-10-517-441-283
; Sequence 283, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 283
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-517-441-283

Query Match      15.2%; Score 106.6; DB 6; Length 8666;
```

```
Best Local Similarity 49.0%; Pred. No. 3.2e-10;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

QY 12 AAAGTTTTTTTTTTTGATGATTTTAAATAAAATATACATTTCTTTTATTATTATTAT 71
DB 1547 AAAGTTTTTTTTTTTGATGATTTTAAATAAAATTTTAAATTTTAAATTTTAAATTTTAA 1606

QY 72 ACTTTTAAGTTTTAGGTACATGTGCAAGGTGTCAGGTAGTTACATATATATACATGT 131
DB 1607 TATTTTAAAGTTTTAGAGATATATGTGTAAATGTGTAGGTGTGTATATATATATATATGT 1666

QY 132 GCATCTGCTGCTGCACCATTAATCACTCAATGAAGTTTTTTTTTAAATTTTGTAGTACA 191
DB 1667 GTTATGTTGGTGTGTGTATTTATTAATTTA-TTATTTAGTATTAGGTATATTTTAAAT 1725

QY 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATAAATCAATCAATTTGAAAAAATGT 251
DB 1726 GTTATTTTCTTTTCTTTTATATAAGATTTTAAATGGAATGGAATTTTAAATTTT 1785

QY 252 TAACACTCTGATATAAAAGTTTTTATAGTTTCTCTACTTTTAAAGCAAAATCCATAGGCA 311
DB 1786 AGAGTAAATGGTTTTTATTTAAAGGATGTTATAATTTTTTTTAGAGTTTATTTGTAAGATAT 1845

QY 312 TGTAAATCTAGTTTCAACATTTACTTGCAGTTTTCAGTTAGTAAATAAATTAAGCTAG 371
DB 1846 GAGATATATATTTAAATTTGTTTTCGTATTTTAAAGTAGTTAAATTTTATATTG 1905

QY 372 TAAGTATAATTTAATTTGTCAAATTAATTTGGAATAATACATGGGTACTTAATTTGATTT 431
DB 1906 TTTATAATGTATTTAAATGTTGTTTTTATATGTTGTTATTTTATTTTATTTTAAATA 1965

QY 432 ACCAAATTTCCATGGGAACAACAAGTTGCTATTTTTTGGATTGATATTTTGAATACT 491
DB 1966 GTTATATATATTTTATTAAGAGTTGAAAGAGTTTGTAGTAGGAATTTATGTTAGAT 2025

QY 492 AGTACAGGAATATCATTTGTTAGTTGAATTTTTCAGCTTAGAATAAATAAGAGTTAGAT 551
DB 2026 TTTAGAGAAATTTTGAATTTTATGAAAGTTTATTTAGAAATATATATGTTAGTGAATA 2085

QY 552 AGCTAAAGTATAATTTTATTTGATTTTAATTAATGATGAGTTAGGTAGGTATGATTAATTA 611
DB 2086 TATTTTTTTTAAAAAAATTAATTTATTTTATTTTTCGAGAAAGGTTATTTATTTTA 2145

QY 612 GTGAAAACACCCCAAGATGTTTATATCTTTTAAATTT 648
DB 2146 ATAGATTTTGAAGGAGTTTATTTTATTTTATTTT 2182

RESULT 3
US-10-517-441-557
; Sequence 557, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
```

```
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 557
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-557

Query Match      15.2%; Score 106.6; DB 6; Length 8666;
Best Local Similarity 49.0%; Pred. No. 3.2e-10;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

Qy 12 AAAAGTTTTTTTTTTTGATGATTTTAAATAAAATATCATTTTCTTTTTTATTATTAT 71
Db 1547 AAAGTTTTTTTATTATTATTAAATTATTTATATATATTTTAAATTTTATTATTATTA 1606

Qy 72 ACTTTTAAAGTTTGGGACATGCGCAAAGTGTGCAGGTAGTTACATATATATACATGT 131
Db 1607 TATTTTAAAGTTTGGGACATGCGCAAAGTGTGCAGGTAGTTACATATATATATATGT 1666

Qy 132 GCCATGCTGTGTGCTGCACCCATTAACATCAGTGTCTTTTAAATTTTAGTGACA 191
Db 1667 GTTATGTTGGTGTGTGTTATTTTAAATTTA-TTATTTAGTATTAGGTATATATTTTAAAT 1725

Qy 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATAGTAATCATATAAATTTGAAAAAATGT 251
Db 1726 GTTATTTTCTTTTCTTTTATATAAGATTTTATATGATTAATGATTTTAAATTTT 1785

Qy 252 TAACACTCTGATAAAAAAGTTTATAGTTTCCACTTTTAAAGCAAAATCCATAGGGCA 311
Db 1786 AGAGTAAATGGTTTATTTAAGGATGTTATAAATTTTGTAGAGTTTATTTGTAAGATAT 1845

Qy 312 TGGTAATGTAGTTTCAACATTTACTTGCAGTTTCCAGTTAGTTAAATAAATTAAGCCTAG 371
Db 1846 GAGATATATATATTTAAAAATTTGTTTGGTATTTTAAAGTAGTTAAATTTTATATTTG 1905

Qy 372 TAAGTATAAATTAATTTGTCAAATAATTTGCAAAATACCATGGTACTTAATGATTTT 431
Db 1906 TTTATATGATTTTAAAGTTGTTTATATATGTTGTATTTTATTTTATTATTATAA 1965

Qy 432 ACCAAATTTCCATGGAACAAACAAGTTGGCTATTTTGGATTTGATATTTTGAATACT 491
Db 1966 GTTATATATATTTTATTAAGAGTTGAAAGAGTTTTCATGTAGGAATTTATGGTAGAGT 2025

Qy 492 AGTACAGGAATATCATTTGTTAGTTGAATTTTTCAGCTTAGAAAACAATGGAGTTAGAT 551
Db 2026 TTTAGAGAAATTTTGTGAATTTATTTGAAAGTTTATTTTAGAATAATATGTGTGAAGTGAATA 2085

Qy 552 AGCTAAAGTATAAATTTATTTGTGATTTAAATAGTATGAGTTAGGCTATGATAATTA 611
Db 2086 TATTTTATTTTAAAAAATTAATTTATTTTATTTTATTTTATTTTGGAGAAGGATTTATTATTTA 2145

Qy 612 GTGAAACACCCCAAGATGTTTTTACTTTTTAAATTT 648
Db 2146 ATAGATTTTGAAGGAGTTTATTTTATTTTATTTT 2182

RESULT 4
US-10-539-228-214
; Sequence 214, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (PP023370.0003)
```

```
; CURRENT APPLICATION NUMBER: US/10/539,228
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 72678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-539-228-214

Query Match      14.9%; Score 104.6; DB 6; Length 72678;
Best Local Similarity 80.8%; Pred. No. 8.7e-10;
Matches 122; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 11 TAAAGTTTTTTTTTTTGATGATTTTAAATAAAATATCATTTTCTTTTTTATTATTATTA 70
Db 68541 TACAGAACTCTTTTTTTTTTTTTTTTTCATTTCTCTCTATATATTTTTTATTATTATTA 68600

Qy 71 TACTTTTAAAGTTTGTAGGTACATGTCAAAAGTGTGCAGGTAGTTACATATATATACATG 130
Db 68601 TACTTTTAAAGTTTGTAGGTACATGTCACAAATGTCAGGTAGTTACATATATATACATG 68660

Qy 131 TGCATGCTGTGTGTGCTGCACCCATTAATC 161
Db 68661 TGCATGCTGTGTGCTGCACCCGCTAACTC 68691

RESULT 5
US-10-505-928-596
; Sequence 596, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 596
; LENGTH: 70665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-596

Query Match      14.8%; Score 103.4; DB 6; Length 70665;
Best Local Similarity 87.6%; Pred. No. 1.4e-09;
Matches 113; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 33 TTTTAAATAAATAATCATTTTCTTTTTTATTATTATTATTTTAAAGTTTACGGTACA 92
Db 62754 TTTTTTTTTTGAGTTTCTTTTTTTTAAATTATTATTATCTTTTAAAGTTTACGGTACA 62813

Qy 93 TGTGCAAGTGTGCAGGTAGTTACATATATATACATGTCCTGCTGCTGCACCC 152
Db 62814 TGTGCAAAATGTGCAGGTAGTTACATATATATATATATGTCATGTCCTGCTGCTGCACCC 62873

Qy 153 CATTAACCTC 161
Db 62874 CATTAACCTC 62882

RESULT 6
US-11-266-748A-58095/c
; Sequence 58095, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
```

APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 58095
LENGTH: 1615
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-58095

Query Match 14.5%; Score 101.6; DB 8; Length 1615;
Best Local Similarity 86.1%; Pred. No. 2.1e-09;
Matches 124; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
Qy 18 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTTT 77
Db 1615 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTTT 1557
Qy 78 AGTTTTCAGGTACATGCAAGTGTGCAGGTAGTTACATATATATATATGCGCATG 137
Db 1556 AAGTTTTCAGGTACATGCAAGTGTGCAGGTAGTTACATATATATATATGCGCATG 1497
Qy 138 CTGCTGTGCTGCCACCCCAATTAATC 161
Db 1496 CTGCTGTGCTGCCACCCCAATTAATC 1473

RESULT 7
US-11-266-748A-25751/c
Sequence 25751, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25751
LENGTH: 1577
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-25751
Query Match 14.3%; Score 100.4; DB 8; Length 1577;
Best Local Similarity 84.9%; Pred. No. 3.4e-09;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 16 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTTT 75
Db 1573 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTTT 1515
Qy 76 TTAAGTTTTCAGGTACATGTCAGGTAGTTACATATATATATATATGCGCA 135
Db 1514 TTAAGTTTTCAGGTACATGTCAGGTAGTTACATATATATATATGCGCA 1455
Qy 136 TGCTGTGCTGCCACCCCAATTAATC 161
Db 1454 TGCTGTGCTGCCACCCCAATTAATC 1429

RESULT 8
US-11-266-748A-197923
Sequence 197923, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 197923
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-197923

Query Match 14.3%; Score 99.8; DB 8; Length 1000;
Best Local Similarity 73.1%; Pred. No. 4.1e-09;
Matches 128; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 2 TGTTCACATAAAGTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTCTTTT 61
Db 421 TGTTCACATAAAGTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTCTTTT 480


```

; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23292
; LENGTH: 122568
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23292

Query Match      14.2%; Score 99.6; DB 8; Length 122568;
Best Local Similarity 81.0%; Pred. No. 6.8e-09;
Matches 128; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY      4  TTTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATACATTTTCTTTTATT 63
Db      6843 TTTATTCCTATTTTTTTTTCTTTTTTTTTTTTTTTTGTAGTTTCTTTTTTTTCTTTT 6902

QY      64  ATTATTATACCTTTTAAGTTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATAT 123
Db      6903 ATTATTATAC-TTTTAAGTTTTTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGT 6961

QY      124  ATACATGTGCCATGCTGGTGTGCTGCACCCCACTAACTC 161
Db      6962 ATACATGTGCCACGCTGGTGCCTGCACCCCACTAACTC 6999

RESULT 12
US-11-266-748A-205304
; Sequence 205304, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 205304
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-205304

Query Match      14.2%; Score 99.2; DB 8; Length 1000;
Best Local Similarity 76.2%; Pred. No. 5.2e-09;
Matches 122; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY      2  TGTTCACATAAAGTTTTTTTTTTTTCATCATTTTAATAAAATACATTTTCTTTTTTA 61
Db      609  TGTTCATTCATGATTTTCTTTTTTTTATTTATTTACTATTATTATTTTATTATTATT 668

QY      62  TTATTATTACTTTTAAAGTTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATAT 121

```


! LENGTH: 131546
! TYPE: DNA
! ORGANISM: Homo Sapiens
US-11-266-748A-60109

Query Match 13.9%; Score 97; DB 8; Length 131546;
Best Local Similarity 75.2%; Pred. No. 2e-08;
Matches 121; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 CTTTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTT 60
DB 91001 CAGTCTAGTACAAACCGAAGTGTAAATGCAATCAATAGTTTCTTTTTTAATTT 91060
QY 61 ATTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATA 120
DB 91061 TTTTAAATTATTTTAAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATA 91120
QY 121 TATATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTC 161
DB 91121 TGTATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTC 91161

RESULT 21

US-11-266-748A-290116
; Sequence 290116, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 290116
; LENGTH: 1000
; TYPE: DNA

; ORGANISM: Homo Sapiens
US-11-266-748A-290116

Query Match 13.8%; Score 96.8; DB 8; Length 1000;
Best Local Similarity 79.4%; Pred. No. 1.4e-08;
Matches 127; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTTA 61
DB 443 TGTATATAAAACCGGTTTATTTCTCTATTACATATCTCTTTTCTTGTTTTTA 502
QY 62 TTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATAT 121
DB 503 TTATTATTATAC-TTTAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATAT 561
QY 122 ATATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTC 161
|||||

DB 562 GTATACATGTGCCATATTGGTGTGCTGCACCCATTAACCTC 601

RESULT 22

US-11-266-748A-341545/c
; Sequence 341545, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 341545
; LENGTH: 1000
; TYPE: DNA

; ORGANISM: Homo Sapiens
US-11-266-748A-341545

Query Match 13.8%; Score 96.8; DB 8; Length 1000;
Best Local Similarity 79.4%; Pred. No. 1.4e-08;
Matches 127; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTTA 61
DB 558 TGTATATAAAACCGGTTTATTTCTCTATTACATATCTCTTTTCTTGTTTTTA 499
QY 62 TTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATAT 121
DB 498 TTATTATTATAC-TTTAAGTTTAAAGGTACATGTGCAAAAGTGCAGGTAGTTACATAT 440
QY 122 ATATACATGTGCCATGTGGTGTGCTGCACCCATTAACCTC 161
|||||

RESULT 23

US-11-266-842-1/c
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:

; APPLICANT: Vance, Jeffrey M.
; APPLICANT: Kraus, William E.
; APPLICANT: Goldschmidt, Pascal J.
; APPLICANT: Gregory, Simon G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
; FILE REFERENCE: 5405-347
; CURRENT APPLICATION NUMBER: US/11/260,842
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/662,447
; PRIOR FILING DATE: 2004-10-27

```
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 261789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-260-842-1

Query Match      13.8%; Score 96.8; DB 8; Length 261789;
Best Local Similarity 84.0%; Pred. No. 2.3e-08;
Matches 121; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 17 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATATATATATATTT 76
Db 257725 TTTTCTTTTGGAGTGCCTGAAGATTTTCAACTTTCTTTTATATATATAT 257667

QY 77 TAAAGTTTAAAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCAT 136
Db 257666 TAAAGTTTAAAGGTACATGTGCACAAATGTGCAGGTAGTTACATATGTATACATGTGCCAT 257607

QY 137 GCTGGTGTGTCACCCCAATTAAC 160
Db 257606 GCGGGTGCCTGCACCCCACTAACT 257583

RESULT 24
US-11-266-748A-28210/c
; Sequence 28210, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117289
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-117289

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATATATATATTTACT 75
Db 986 TTTTCTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATATATATTTTACT 927

QY 76 TTAAGTTTAAAGGTACATGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 926 TTAAGTTTAAAGGTACATGTGCACAACTGCAGGTGTGTACATATGTATACATGTGCCA 867

QY 136 TCGTGTGTGCTGCACCCCAATTAAC 161
Db 866 TGGTGTGTGCTGCACCCCAATTAAC 841

RESULT 26
US-11-266-748A-159453
; Sequence 159453, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
```

```
QY 136 TCGTGTGTGCTGCACCCCAATTAAC 159
Db 48674 TCGTGTGTGCTGCACCCCAATTAAC 48651

RESULT 25
US-11-266-748A-117289/c
; Sequence 117289, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117289
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-117289

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATATATATTTACT 75
Db 986 TTTTCTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATATATTTTACT 927

QY 76 TTAAGTTTAAAGGTACATGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 926 TTAAGTTTAAAGGTACATGTGCACAACTGCAGGTGTGTACATATGTATACATGTGCCA 867

QY 136 TCGTGTGTGCTGCACCCCAATTAAC 161
Db 866 TGGTGTGTGCTGCACCCCAATTAAC 841

RESULT 26
US-11-266-748A-159453
; Sequence 159453, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
```

```
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159453
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-159453

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 75
DB 15 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 74
QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 75 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATATGTATACATGTGCCA 134
QY 136 TCGTGGTGTGCTGCCACCCATTAACCTC 161
DB 135 TGGTGGTGTGCTGCCACCCATTAACCTC 160

RESULT 27
US-11-266-748A-288898/c
; Sequence 288898, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288898
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 75
DB 15 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 74
QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 75 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATATGTATACATGTGCCA 134
QY 136 TCGTGGTGTGCTGCCACCCATTAACCTC 161
DB 135 TGGTGGTGTGCTGCCACCCATTAACCTC 160
```

```
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 75
DB 96 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 927
QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 926 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATATGTATACATGTGCCA 867
QY 136 TCGTGGTGTGCTGCCACCCATTAACCTC 161
DB 866 TGGTGGTGTGCTGCCACCCATTAACCTC 841

RESULT 28
US-11-266-748A-340327
; Sequence 340327, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 340327
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-340327

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 75
DB 15 TTTTCTTTTGTGATGATTTTAAATAATATCATTTCTTTTATTTATTTATTTACTT 74
QY 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 75 TTAAGTTTGTAGGTACATGTGCACACGTGCAGGTTGTACATATATGTATACATGTGCCA 134
QY 136 TCGTGGTGTGCTGCCACCCATTAACCTC 161
DB 866 TGGTGGTGTGCTGCCACCCATTAACCTC 841
```

```
Db 135 TGGTGGTGTGTCACCCATTAACTC 160
;
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470871
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-470871

Query Match 13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db 15 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 74
QY 76 TTAAGTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 135
Db 75 TTAAGTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 134
QY 136 TCGTGGTGTGTCACCCATTAACTC 161
Db 135 TGGTGGTGTGTCACCCATTAACTC 160

RESULT 31
US-10-506-549-3
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 13.8%; Score 96.4; DB 6; Length 394191;
Best Local Similarity 78.8%; Pred. No. 2.8e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db 136948 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 137007
QY 76 TTAAGTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 135
```

```
Db 135 TGGTGGTGTGTCACCCATTAACTC 160
;
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470871
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-470871

Query Match 13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db 986 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 927
QY 76 TTAAGTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 135
Db 926 TTAAGTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 867
QY 136 TCGTGGTGTGTCACCCATTAACTC 161
Db 866 TGGTGGTGTGTCACCCATTAACTC 841

RESULT 30
US-11-266-748A-470871
; Sequence 470871, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
```


;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700,293
;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 220785
;; LENGTH: 1000
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-11-266-748A-220785

Query Match 13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTTATTTATTTATTTACT--T 75
Db 465 TTGTTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTACT 524

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTACATATATATATATATATATGCGCA 135
Db 525 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTACATATGATATATATATGCGCA 584

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db 585 TGCTGGTGTGCTGCACCCATTAACTC 610

RESULT 38
US-11-266-748A-284468
; Sequence 284468, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 284468
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-284468

Query Match 13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTTATTTATTTATTTACT--T 75
Db 465 TTGTTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTACT 524

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTACATATATATATATATATATGCGCA 135
Db 525 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTACATATGATATATATATGCGCA 584

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db 585 TGCTGGTGTGCTGCACCCATTAACTC 610

RESULT 39
US-11-266-748A-335897/c
; Sequence 335897, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 335897
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-335897

Query Match 13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTTATTTATTTATTTACT--T 75
Db 536 TTGTTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTACT 477

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTACATATATATATATATATATGCGCA 135
Db 476 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTACATATGATATATATATGCGCA 417

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db 416 TGCTGGTGTGCTGCACCCATTAACTC 391

RESULT 40
US-11-266-748A-394477
; Sequence 394477, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same

```
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394477
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-394477
```

```
Query Match      13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY      18  TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACT--T 75
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      465  TTGTTTATTATTATTATTTTAAATTTTAAATTTTATTTATTTATTTATTTACT 524

QY      76  TTAAGTTTGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      525  TTAAGTTTGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTACATGTGCCA 584

QY      136  TGTGTGTGCTGCACCACTTAATCT 161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      585  TGTGTGTGCTGCACCACTTAATCT 610
```

```
RESULT 41
US-11-266-748A-465523/c
; Sequence 465523, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
```

```
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465523
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-465523

Query Match      13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY      18  TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACT--T 75
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      536  TTGTTTATTATTATTATTTTAAATTTTAAATTTTATTTATTTATTTATTTACT 477

QY      76  TTAAGTTTGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      476  TTAAGTTTGGGTACATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCA 417

QY      136  TGTGTGTGCTGCACCACTTAATCT 161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      416  TGTGTGTGCTGCACCACTTAATCT 391

RESULT 42
US-11-347-766-75/c
; Sequence 75, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCR/US
; CURRENT APPLICATION NUMBER: US/11/347,766
; CURRENT FILING DATE: 2006-02-02
; PRIOR APPLICATION NUMBER: US/10/433,287
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 22884
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: genomic DNA
; LOCATION: (1)..(22884)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, or dTTP)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9562)..(9621)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: initial coding region
; LOCATION: (12238)..(12393)
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (13544)..(13681)
; FEATURE:
; NAME/KEY: coding region
; LOCATION: (15338)..(15394)
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (18027)..(18188)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18413)..(18436)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (19594)..(19695)
; FEATURE:
```


Db 18938 GTTTTTTTTCCCTGTTTCCACCTCTTTTTTTTTTCTTTTTTTTTTTTATTAT 18997
QY 75 --TTTAAAGTTTGGGTACATGCAAAAGTGTGCAGGTTAGTTACATATATACATG 132
Db 18998 ACTTTAAGTTTGGGTACATGTCACCTTGTGCAGGTTAGTTACATATGTTACATG 19057
QY 133 CCATGCTGCTGTGCTGCACCCCACTTAAC 161
Db 19058 CCATGCTGCTGCTGCACCCCACTTAAC 19086

RESULT 48
US-11-175-714-86
; Sequence 86, Application US/11175714
; Publication No. US20060122373A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; APPLICANT: Busfield, Samantha J.
; APPLICANT: Barnes, Thomas M.
; APPLICANT: Mackay, Charles
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,
; TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: MPI05-0100NMNIM
; CURRENT APPLICATION NUMBER: US/11/175,714
; PRIOR FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 10/417,719
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: US 09/832,633
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: US 10/895,676
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: US 10/105,934
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/862,972
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 09/062,389
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 09/062,017
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/044,746
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-11-175-714-86

Query Match 13.6%; Score 95; DB 8; Length 152331;
Best Local Similarity 76.8%; Pred. No. 4.5e-08;
Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTTTTATTATTA 70
Db 13565 TATTTTATTTTATTTTATTTATTTATTTTAAATTTTTTAAATTTTAAAT 135624
QY 71 TACTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATG 130

Db 135625 ATGCTTTTAAAGTTTGGGTACATGTGCAATTTGTGCAGGTTAGTTACATACGCATACATG 135684
QY 131 TGCATGCTGCTGTGCTGCACCCCACTTAAC 161
Db 135695 CGCCATGCTGCTGCTGCACCCCACTTAAC 135715

RESULT 49
US-11-175-714-87
; Sequence 87, Application US/11175714
; Publication No. US20060122373A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; APPLICANT: Busfield, Samantha J.
; APPLICANT: Barnes, Thomas M.
; APPLICANT: Mackay, Charles
; APPLICANT: Lora, Jose M.
; TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,
; TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: MPI05-0100NMNIM
; CURRENT APPLICATION NUMBER: US/11/175,714
; PRIOR FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 10/417,719
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/872,855
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: US 09/832,633
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: US 10/895,676
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: US 10/105,934
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/862,972
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 09/062,389
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/062,017
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/044,746
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-11-175-714-87

Query Match 13.6%; Score 95; DB 8; Length 176373;
Best Local Similarity 76.8%; Pred. No. 4.5e-08;
Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTTTTATTATTA 70
Db 148145 TATTTTATTTTATTTTATTTATTTTAAATTTTTTAAATTTTTTAAAT 148204
QY 71 TACTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATACATG 130
Db 148205 ATGCTTTTAAAGTTTGGGTACATGTGCAATTTGTGCAGGTTAGTTACATACGCATACATG 148264

Qy 131 TGCATGCTGGTGTGCTGCACCCATAACTC 161
Db 148265 CGCCATGCTGGTGGCTGCACCCATAACTC 148295

RESULT 50
US-11-266-748A-28223
; Sequence 28223, Application US/11266748A
; Publication No. US20050134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28223
; LENGTH: 495475
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14152)..(14163)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14173)..(14173)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20582)..(20681)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21980)..(21980)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21992)..(21992)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42256)..(42256)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42260)..(42260)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42263)..(42263)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (202648)..(202648)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202661)..(202661)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202663)..(202663)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202671)..(202672)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202680)..(202680)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202684)..(202684)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202686)..(202686)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202691)..(202691)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202696)..(202697)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202701)..(202702)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202712)..(202714)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448497)..(448497)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448499)..(448500)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448538)..(448538)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-28223

Query Match 13.6%; Score 95; DB 8; Length 495475;
Best Local Similarity 76.8%; Pred. No. 5e-08;
Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 11 TAAAGTTTTTTTTTGGATTTTAAATAAATAATCATTTCTTTTTTATTATTATTA 70
Db 199353 TATTTATTTTTTATTTTATTTATTTATTTATTTTAAATTTTTTAAATTTTAAATTT 199412
Qy 71 TACTTTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATATACATG 130
Db 199413 ATGCTTTAAGTTTGGGTACATGTGCACATTGTGCAGGTTAGTTACATACGCATACATG 199472
Qy 131 TGCATGCTGGTGTGCTGCACCCATAACTC 161
Db 199473 CGCCATGCTGGTGGCTGCACCCATAACTC 199503


```
QY 2 TGTTCACATAAGTTTTTTTTTTTGTGATGATTTTAATAAATATCAATTTCTTTTTTTA 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19640 TTTTTCATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCTTTT 19699

QY 62 TTATTTATATCTTTTAAAGTTTAGGGTACATGTCGCAAGTGTGCAGGTTAGTTACATAT 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19700 TTTTATTTATATCTTTTAAAGTTTAGGGTACATGTCGCAATGTGCAGGTTAGTTACATAT 19759

QY 122 ATATCATGTGCATGCTGGTGTGCTGCACCCATTAATCTC 161
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19760 GTATACATGTGCCATGCTGGTGGCTGCACCCCACTAACTC 19799

RESULT 55
US-11-266-748A-50139
; Sequence 50139, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50139
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-50139

Query Match 13.4%; Score 94; DB 8; Length 630;
Best Local Similarity 76.7%; Pred. No. 4.1e-08;
Matches 115; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 12 AAAGTTTTTTTTTTTGTGATGATTTTAATAAATATCAATTTCTTTTTTTATTTAT 71
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ACAAGTTTTCGGTCTCTTAATATATACCTAGTTGAGTCTCTATTTATTTTATAT 188

QY 72 ACTTTTAAAGTTTTCAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATATATACATGT 131
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 ACTTTTAAAGTTTTCAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATATGATAT 248

QY 132 GCCATGCTGGTGTGCTGCACCCATTAATCTC 161
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 GCCATGTTGGTGTGCTGCACCTGGTTAACTC 278

RESULT 56
US-11-266-748A-202832/c
; Sequence 202832, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
```

```
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 202832
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-202832

Query Match 13.4%; Score 94; DB 8; Length 1000;
Best Local Similarity 87.7%; Pred. No. 4.3e-08;
Matches 114; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 33 TTTTAATAAATAATATCATTTTCTTTTTTTTATTTATTTATTTATTTAAAGTTTAGGGTACA 92
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 803 TTTCACAACATCACCTCTTTTATTATTATTATTATTATTATTATTATTATTATAC-TTTAAGTTTAGGGTACA 745

QY 93 TGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTCGCAATGCTGGTGTGCTGCACC 152
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 744 TGTGCGCAATGTGCAGGTTAGTTACATATGTTACATATGTTACATGCTGGTGTGCTGCACC 685

QY 153 CATTAACCTCA 162
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 684 CATTAACCTCA 675

RESULT 57
US-11-266-748A-23474
; Sequence 23474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
```

```
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23474
; LENGTH: 347503
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23474

Query Match      13.4%; Score 93.8; DB 8; Length 347503;
Best Local Similarity 83.7%; Pred. No. 7.9e-08;
Matches 118; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy 21 TTTTGTGATGATTTTAAATAATATCATTTCTTTTATTATTATTATTATTATTAAAG 80
Db 334107 TTTTATTATTATTTTCGACTCTTTTATTATTATTATTATTATTATATAC-TTTAAG 334165

Qy 81 TTTTAGGTTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTG 140
Db 334166 TTTTAGGTTACATGTGCACATGTGCAGGTAGTTACATATGTATACATGTGCCATGCTG 334225

Qy 141 GTGTGCTGCACCCATTAACTC 161
Db 334226 GTGTGCTGCACCCATTAACTC 334246
```

```
RESULT 58
US-11-266-748A-23170
; Sequence 23170, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23170
; LENGTH: 170452
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3381)..(3381)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3384)..(3384)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (3392)..(3392)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3400)..(3400)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3406)..(3407)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3423)..(3423)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3446)..(3446)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3545)..(3545)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3905)..(3905)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3907)..(3907)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3909)..(3909)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3922)..(3922)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3924)..(3924)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3927)..(3927)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15605)..(15605)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (144156)..(144156)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-23170

Query Match      13.4%; Score 93.6; DB 8; Length 170452;
Best Local Similarity 80.3%; Pred. No. 7.9e-08;
Matches 122; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

Qy 11 TAAAGTTTTTTTTTTTGTGATTTTAAATAAATAATATCATTTCTTTTATTATTATTATTA 70
Db 122784 TAATCTTTTCTTAATCTTACCAATTAATTTTCTTTTAAATTTTATTATTATTATTA 122843

Qy 71 TACTTTTAAAGTTTtaggtacatgtgcaagtgtaggtacatgtacatgtacatgtacatgt 130
Db 122844 TAC-TTTAAGTTTtaggtacatgtgcaagtgtaggtacatgtacatgtacatgtacatgt 122902

Qy 131 TGCCATGCTGGTGTGCTGACCCCACTCA 162
Db 122903 TGCCATGTTGGTGTGCTGACCCCACTCA 122934
```



```
Query Match      13.3%; Score 93.2; DB 8; Length 176928;
Best Local Similarity 78.5%; Pred. No. 9.3e-08;
Matches 124; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 TTTACATAAGTTTTTTTTTTTGATGATTTTAAATAAAATATCAATTTCTTTTATT 63
Db 102485 TTGCATAAAATCTTTTGTCTGTTCTATTAATCTATTTTCTTCTCTTTATT 102544

QY 64 ATTATTATACTTTAAAGTTTATAGGTACATGTGCAAGTGTCAGGTAGTTACATAT 123
Db 102545 ATTATTATAC-TTTAAAGATTAGGTACATGTGCACAATGTCAGGTAGTTACATATGT 102603

QY 124 ATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 102604 AAACAATGTCCATGCTGTGCTGTCGCCACCACTAACAC 102641

RESULT 62
US-11-266-748A-29039
; Sequence 29039, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29039
; LENGTH: 909203
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29039

Query Match      13.3%; Score 93.2; DB 8; Length 909203;
Best Local Similarity 78.1%; Pred. No. 1.1e-07;
Matches 125; Conservative 0; Mismatches 33; Indels 2; Gaps 1;

QY 4 TTTACATAAGTTTTTTTTTTTGATGATTTTAAATAAAATATCAATTTCTTTTATT 63
Db 255117 TTTACTATATTTTATTTTATTTTGTAAATTTTATTTTATTTTCTATGATTATTTT 255176

QY 64 ATTATTATAC-TTTAAAGTTTATAGGTACATGTGCAAGTGTCAGGTAGTTACATAT 121
Db 255177 ATTATTATATAC-TTTAAAGTTTATAGGTACATGTGCAATGTGTCAGGTAGTTACATAT 255236

QY 122 ATATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 255237 GTATACATGTGCCATGCTGTGCTGTCGCCACCACTAACCTC 255276

RESULT 63
US-11-266-748A-211402
; Sequence 211402, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29039
; LENGTH: 909203
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-211402

Query Match      13.3%; Score 93; DB 8; Length 607;
Best Local Similarity 94.7%; Pred. No. 6.1e-08;
Matches 107; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 49 TTTCTTTTTTTTATTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGTGCAAGTGTGCAG 108
Db 4 TTTTTTTTTTTTATTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGTGCAATGTGCAG 62

QY 109 GTTAGTTACATATATATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 63 GTTAGTTACATATGTATATACATGTGCCATGCTGTGCTGCTACACCCATTAACTC 115

RESULT 64
US-10-519-335-37
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

```
LOCATION: (10)..(10)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (60402)..(60402)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (61110)..(61110)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (98207)..(98207)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (98208)..(98208)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (98209)..(98209)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (98210)..(98210)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (98211)..(98211)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (99743)..(99743)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (108055)..(108055)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (109094)..(109094)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (109125)..(109125)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (118900)..(118900)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (119024)..(119024)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (119053)..(119053)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (119115)..(119115)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (119123)..(119123)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (141674)..(141674)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (142063)..(142063)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (142137)..(142137)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (142967)..(142967)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (143077)..(143077)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (143506)..(143506)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (143587)..(143587)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (143629)..(143629)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (149079)..(149079)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (5363)..(5363)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (8080)..(8080)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (10296)..(10296)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (14528)..(14528)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (15336)..(15336)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (15457)..(15457)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (16288)..(16288)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (16306)..(16306)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (16316)..(16316)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (16397)..(16397)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c or g or t
```



```
Db 61651 CTGTCGGCAAAACATCTTTTTTTTTTTGGTCTTTATTATTATTATTATTATT 61710
Qy 61 ATTATTATTATCTTTTAAAGTTTATAGGTACATGTGCAAGTGCAGGTAGTTACATA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61711 ATTATTATTATAC-TTTAAGTTTATAGGTACATGTGCAATGTGCAGGTAGTTACATA 61769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 TATATACATGTGCCATGCTGGTGTCTGCACCCATTAACCTC 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61770 TGTATACAGGTGCCATGATGGTGTGCTGCATCCATTAACTC 61810

RESULT 67
US-11-266-748A-200842/c
; Sequence 200842, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; CURRENT APPLICATION NUMBER: US/11/266,748A
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200842
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-200842

Query Match 13.3%; Score 92.8; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 6.9e-08;
Matches 123; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 5 TTCACATAAAGTTTCTTTTGTGATGATTTTAAATAAATATCATCTTCTTTTATTA 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 155 TTTAAACATTTTGTATGATTTTAAATACAGGAGTAGTATTTCTTTTAAATTTATTA 96
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 65 TTATTATACCTTTTAAAGTTTATAGGTACATGTGCAAGTGCAGGTAGTTACATATATA 124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 95 TTATTATAC-TTTAAGTTTATAGGTACATGTGCAATGTGCAGGTAGTTACATATGTA 37
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 TACATGTGCCATGCTGGTGTCTGCACCCATTAACCT 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 36 TACATGTGCATGCTGGTGTCTGCACCCATTAACCT 1

RESULT 68
US-11-266-748A-25022
; Sequence 25022, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
```

```
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25022
; LENGTH: 38399
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25022

Query Match 13.3%; Score 92.8; DB 8; Length 38399;
Best Local Similarity 89.3%; Pred. No. 9.6e-08;
Matches 100; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 50 TTCTCTTTTATTATTATTTTAACTTTTAACTTTTAAAGTTTATAGGTACATGTGCAAGTGCAGG 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19144 TTTCTTTTATTTTAACTTTTAACTTTTAAAGTTTATAGGTACATGTGCAATTTGTCAGG 19203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 110 TTAGTTACATATATATACATGTGCATGCTGGTGTGTCACCCCACTTAACCTC 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19204 TTAGTTACATATGTATACATGTGCATGCTGGTGTGTCACCCCACTTAACCTC 19255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 69
US-11-266-748A-23809
; Sequence 23809, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23809
; LENGTH: 19204
; TYPE: DNA
; ORGANISM: Homo Sapiens
```

```
; SEQ ID NO 23809
; LENGTH: 39638
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23809
Query Match 13.2%; Score 92.6; DB 8; Length 39638;
Best Local Similarity 72.7%; Pred. No. 1e-07; Indels 1; Gaps 1;
Matches 133; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
```

```
Qy 1 CTGTTTCACATAAAGTTTTTTTTTTTGGATCAATTTTAAATAAATATCAATTTCTTTTTT 60
Db 20025 CTGTTTTCCTTTCTTTTTTTTTTTTGAATATGCTCTTTTTTTTAAATTT 20084
Qy 61 ATTATTATTATACATTTTAAAGTTTGTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATA 120
Db 20085 TTTTATTATTAC-TCTAAGTTTGTAGGGTACATGTGCACATTTGTCAGGTTAGTTACATA 20143
Qy 121 TATATACATGTGCCATGCTGCTGCTGCACCCATTAACTACATGAAGTTTTTTTTTAAA 180
Db 20144 TGTATACATGTGCCATGCTGCTGCTGCACCCACTAACGTGTCTAGCATTAGGTATA 20203
Qy 181 TTT 183
Db 20204 TCT 20206
```

```
RESULT 70
US-11-266-748A-60803/c
; Sequence 60803, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60803
; LENGTH: 176928
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24475)..(24476)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-60803
```

```
Query Match 13.2%; Score 92.6; DB 8; Length 176928;
Best Local Similarity 82.5%; Pred. No. 1.2e-07; Indels 1; Gaps 1;
Matches 118; Conservative 0; Mismatches 24; Indels 1; Gaps 1;
```

```
Qy 19 TTTTTCATGATGATTTTAAATAAATATCAATTTCTTTTTTTTATTATTATACATTTTA 78
```

```
Db 145805 TTTATCTTTTATTGTTTAGATTTTATTATTATTATTATTATTATTATTATTATTATT 145747
Qy 79 AGTTTGTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTAGTTACATATATATACATGTC 138
Db 145746 AGTTTGTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTAGTTACATATATGTCGCTGT 145687
Qy 139 TGGTGTGCTGTCACCCCAATTAACCTC 161
Db 145686 TGGTGTGCTGTCACCCCAATTAACCTC 145664
```

Search completed: July 19, 2006, 07:13:54
Job time : 291 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 19, 2006, 06:54:08 ; Search time 4403 Seconds
(without alignments)
8890.196 Million cell updates/sec

Title: US-10-661-966-1_146001-146700_A146311
Perfect score: 700
Sequence: 1 ctgtttcacataaagttttt.....gccttttagtgatggtgca 700

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hc1:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	110	15.7	961	4	BX415806	BX415806 BX415806
2	107.4	15.3	785	12	BZ598311	BZ598311 WHADR40TR
3	106.8	15.3	522	11	B52311	B52311 CIT-HSP-388
4	102.8	14.7	375	11	AQ356702	AQ356702 CITBI-E1-
5	102.8	14.7	632	11	AQ195233	AQ195233 RPCI11-48
6	102.6	14.7	567	9	DB349127	DB349127 DB349127
7	102	14.6	397	11	AQ111354	AQ111354 CIT-HSP-2
8	102	14.6	506	9	CX869873	CX869873 HESCA_38
9	102	14.6	552	9	DA104597	DA104597 DA104597
10	101.8	14.5	421	11	AQ884211	AQ884211 HS_5499_B
11	101.8	14.5	681	14	AG102621	AG102621 Pan trogl
12	101.4	14.5	591	11	AQ527159	AQ527159 CITBI-E1-
13	101.2	14.5	524	10	W44804	W44804 zb98G09.s1
14	101.2	14.5	527	11	AQ756779	AQ756779 HS_5407_A
15	100.8	14.4	445	13	CZ457195	CZ457195 MCF740G11
16	100.8	14.4	746	8	CR737970	CR737970 CR737970
17	100.6	14.4	417	11	AQ021610	AQ021610 CIT-HSP-2
18	100.4	14.3	225	4	CB048927	CB048927 NISC_9107
19	100.4	14.3	233	4	CB410332	CB410332 NISC_nc11

20	100.4	14.3	285	11	AQ229797	AQ229797 HS_2033_A
21	100.4	14.3	451	11	AQ109589	AQ109589 CIT-HSP-2
22	100.4	14.3	541	1	AL310239	AL310239 Q07sh12.x
23	100.4	14.3	1577	6	BC010517	BC010517 Homo sapi
24	100.2	14.3	572	11	B72257	B72257 RPCI11-7016
25	100.2	14.3	671	14	CR59536	CR59536 Homo sapi
26	100.2	14.3	870	13	CZ450878	CZ450878 MCF731m05
27	100	14.3	307	1	AA344409	AA344409 EST50301
28	100	14.3	621	4	C947015	C947015 is10a12.y
29	100	14.3	672	11	AQ052012	AQ052012 RPCI11-53
30	100	14.3	677	1	AL601657	AL601657 DKF2p313M
31	99.6	14.2	272	11	AQ266524	AQ266524 RPCI11-75
32	99.4	14.2	352	14	AG189910	AG189910 Pan trogl
33	99.4	14.2	505	9	DA502536	DA502536 DA502536
34	99.4	14.2	548	11	B92240	B92240 RPCI11-20K1
35	99.4	14.2	771	3	BQ007697	BQ007697 UI-H-E10
36	99.4	14.2	906	3	BQ924499	BQ924499 AGENCOURT
37	99.2	14.2	571	11	AQ319769	AQ319769 RPCI11-10
38	99	14.1	401	1	AA446110	AA446110 zw60b03.s
39	99	14.1	464	11	AQ029723	AQ029723 RPCI11-41
40	99	14.1	553	9	DB302517	DB302517 DB302517
41	99	14.1	665	14	AG042325	AG042325 Pan trogl
42	99	14.1	704	11	AQ779743	AQ779743 HS_5571_B
43	98.8	14.1	419	10	Z36956	Z36956 HHEA81M Atr
44	98.8	14.1	424	11	AQ042547	AQ042547 CIT-HSP-2
45	98.8	14.1	468	11	AQ127855	AQ127855 HS_3094_A
46	98.8	14.1	561	11	AQ550918	AQ550918 RPCI-11-3
47	98.8	14.1	725	3	BQ447264	BQ447264 UI-H-EU1-
48	98.8	14.1	853	13	CZ446241	CZ446241 MCF72Sh15
49	98.8	14.1	3088	6	BC032464	BC032464 Homo sapi
50	98.4	14.1	324	11	AQ017761	AQ017761 CIT-HSP-2
51	98.4	14.1	398	11	AQ605001	AQ605001 HS_2119_B
52	98.4	14.1	713	4	BX115372	BX115372 BX115372
53	98.2	14.0	273	3	BUE07283	BUE07283 UI-CF-FN0
54	98.2	14.0	555	11	AZ519511	AZ519511 RPCI-11-3
55	98.2	14.0	560	9	DB097926	DB097926 DB097926
56	98	14.0	226	3	BQ352132	BQ352132 IL3-HT061
57	98	14.0	480	11	AQ628311	AQ628311 CITBI-E1-
58	98	14.0	740	14	CR958489	CR958489 Homo sapi
59	97.8	14.0	385	11	B75832	B75832 RPCI11-12I1
60	97.8	14.0	657	8	CR750736	CR750736 DKF2p470L
61	97.8	14.0	724	11	AF118407	AF118407 AF118407
62	97.6	13.9	513	11	AQ464599	AQ464599 HS_5104_B
63	97.6	13.9	708	13	CZ465237	CZ465237 MCF756K05
64	97.4	13.9	443	11	B72013	B72013 RPCI11-7E20
65	97.4	13.9	661	14	AG121371	AG121371 Pan trogl
66	97.4	13.9	712	13	CZ179389	CZ179389 AC105347C
67	97.4	13.9	725	12	BZ610242	BZ610242 WHADR41TF
68	97.4	13.9	995	6	CR597534	CR597534 full-length
69	97.2	13.9	238	2	BF954789	BF954789 PM3-NN120
70	97.2	13.9	256	1	AI570164	AI570164 to75f07.x

ALIGNMENTS

RESULT 1	BX415806	Homo sapiens	961 bp	linear	EST 03-MAY-2004
LOCUS	BX415806	THYMUS	Homo sapiens	cdna clone	CS0CAP008YE09
DEFINITION	BX415806	3-PRIME, mRNA	sequence.		
ACCESSION	BX415806	GI:46953996			
VERSION	BX415806.2				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo				
REFERENCE	1 (bases 1 to 961)				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				

REFERENCE	Hominidae; Homo.
AUTHORS	1 (bases 1 to 506)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: BresaGen, Inc. CDNA Library Preparation: Express Genomics, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone Distribution: Laboratory for Genomics and Bioinformatics, University of Georgia Found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM15783 row: i column: 08 Seq primer: JENREV (CAGGAACAGCTATGACC) High quality sequence stop: 506.
FEATURES	Location/Qualifiers 1..506 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:7474642" /sex="male" /tissue_type="embryonic stem" /cell_type="human embryonic stem cells" /cell_line="BG01" /lab_host="DH10B-T1 phage-resistant E. coli" /clone_lib="NIH MGC 262" /note="Vector: pExpress-1; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type. Cell line id and NIH Registry designation is BG01. Positive for Nestin and Musashi expression. Passage number 18. cDNA primed using oligo-dT primer: 5'-pGACTAGTTTCAGTCGGAGCGGCCG(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH_MGC_259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Note: this is a Mammalian Gene Collection library."
SOURCE	
ORIGIN	Query Match 14.6%; Score 102; DB 9; Length 506; Best Local Similarity 85.6%; Pred. No. 4,1e-08; Matches 125; Conservative 0; Mismatches 20; Indels 1; Gaps 1; QY 16 TTTT...TTTGTGATGTTTTTAATAAAATATCATTTCTTTTATTATTATTATTT 75 DB 16 TTTT...TTTTTTTTTTTTTTAAAAAATATCTCTTTTATTATTATTAAACTT 75 QY 76 TTAAGTTT...TAGGTACATGTCGCAAGTGTCAGGTTAGTTACATATATACATGTGCCA 135 DB 76 -TAAAGTTT...TAGGTACATGTCGCAAGTGTCAGGTTAGTTACATATGATACATGTGCCA 134 QY 136 TGCTGGTGTGCTGCACCCCAATTAACCT 161 DB 135 TGCTGGTGTGCTGCACCCCAATTAACCT 160 RESULT 9 DA104597 LOCUS DEFINITION DA104597 Homo sapiens CDNA clone BRACE3018053 5', mRNA ACCESSION DA104597 VERSION DA104597.1 GI:78759434
KEYWORDS	EST.
SOURCE	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 552) Kimura.K., Wakamatsu,A., Suzuki.Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii.S., Sugiyama.T., Saito.K., Isono,Y., Irie.R., Kushida.N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,I., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi.H., Nakai.K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes Genome Res. 16 (1), 55-65 (2006) 16344560 Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel.: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@infy.com NEIDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB. Location/Qualifiers 1..552 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="BRACE3018053" /tissue_type="cerebellum" /clone_lib="BRACE3" /note="Vector: pME18P.L3"
FEATURES	Location/Qualifiers 1..552 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="BRACE3018053" /tissue_type="cerebellum" /clone_lib="BRACE3" /note="Vector: pME18P.L3"
ORIGIN	Query Match 14.6%; Score 102; DB 9; Length 552; Best Local Similarity 85.6%; Pred. No. 4e-08; Matches 125; Conservative 0; Mismatches 20; Indels 1; Gaps 1; QY 16 TTTT...TTTGTGATGTTTTTAATAAAATATCATTTCTTTTATTATTATTATTT 75 DB 334 TTAATTTT...TTTATTATTATTATTATTATTATTATTATTATTATTATTAT 392 QY 76 TTAAGTTT...TAGGTACATGTCGCAAGTGTCAGGTTAGTTACATATATACATGTGCCA 135 DB 393 TTAAGTTT...TAGGTACATGTCGCAAGTGTCAGGTTAGTTACATATGATACATGTGCCA 452 QY 136 TGCTGGTGTGCTGCACCCCAATTAACCT 161 DB 453 TGCTGGTGTGCTGCACCCCAATTAACCT 478 RESULT 10 AQ884211 LOCUS DEFINITION AQ884211 Human Male BAC library Homo sapiens genomic_clone Plate=9267 Col=7 Row=N, genomic survey sequence. ACCESSION AQ884211 VERSION AQ884211.1 GI:6315678 KEYWORDS GSS. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 421)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

PUBMED 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 9267 row: N column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 421.

FEATURES

source
1..421
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=9267 Col=7 Row=N"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 14.5%; Score 101.8; DB 11; Length 421;
Best Local Similarity 93.8%; Pred. No. 4.5e-08;
Matches 106; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 49 TTTTCTTTTATTATTATATATATCTTTTAAAGTTTGGGTGACATGCGAAAGTGTGCAG 108
|||||
Db 165 TTTTATTGTTATTATTATATATCTTTTAAAGTTTGGGTGACATGCGAAAGTGTCCG 224
|||||

Qy 109 GTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCCCATTAACCT 161
|||||
Db 225 GTTAGTTACATATGATATACATGTGCCATGCTGGTGTGCTGCCCATTAACCT 277
|||||

RESULT 11
AG102621 681 bp DNA linear GSS 03-NOV-2001

LOCUS Pan troglodytes DNA, clone: PTB-105P19.F, genomic survey sequence.

ACCESSION AG102621

VERSION AG102621.1 GI:167231138

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 681)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission

JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@gs.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>), Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

COMMENT PRIMERS
Sequencing: -21M13

LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI

FEATURES

source
1..681
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-105P19.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 14.5%; Score 101.8; DB 14; Length 681;
Best Local Similarity 81.4%; Pred. No. 4.3e-08;
Matches 118; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 17 TTTTCTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTACTTT 76
|||||
Db 120 TATTTCTTTTATTTTATTTTAAATTTTAAATTTTATTTTATTTTATTTATTTACTT 179
|||||

Qy 77 TAAGTTTGGGTACATGCGAAAGTGTGCAGTTAGTTACATATATATATACATGTGCCAT 136
|||||
Db 180 TAAGTTTGGGTACATGTCACATTTGTCAGGTTAGTTACATATGATACATGTGCCAT 239
|||||

Qy 137 GCTGGTGTGCTGCCCATTAACCT 161
|||||
Db 240 GCTGGTGTGCTGCCCATTAACCT 264
|||||

RESULT 12
AQ527159 591 bp DNA linear GSS 18-MAY-1999

LOCUS CITBI-E1-260411.TF CITBI-E1 Homo sapiens genomic clone 260411, genomic survey sequence.

DEFINITION AQ527159

ACCESSION AQ527159

VERSION AQ527159.1 GI:4838919

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 591)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other GSSs: CITBI-E1-260411.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21

FEATURES	Class: BAC ends.	
	Location/Qualifiers	
	1..591	
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
	/clone="260411"	
	/sex="male"	
	/cell_type="sperm"	
	/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; CalTech Human BAC Library D"	
ORIGIN	Query Match	
	Best Local Similarity 14.5%; Score 101.4; DB 11; Length 591;	
	Matches 117; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	
	16 TTTTCTTTTGTGATGATTTTAATAAAATATCATTTCTTTTATTATTATTATTA	ACTT 75
	405 TATATATTGCTGCTTTTACATTTCTTTCTTTTAAATCTTATTATTATTA	ACTT 464
	76 TTAAGTTTATAGGTACATGTCGAAGTGTGCAGGTAGTACATATATACATG	TGCCA 135
	465 TTAAGTTTATAGGCACATGTGCACAAATGTCAGGTAGTACATATGTA	TATGTTGCCA 524
	136 TCGTGGTGTGCTGCACCCATTAA 158	
	525 TCGTGGTGTGCTGCACCCATTAA 547	
RESULT 13	W44804	
	LOCUS	
	DEFINITION	
	ZB98G09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone	
	IMAGE:320896 3' similar to contains LI.t3 LI repetitive element ;,	
	mRNA sequence.	
	W44804	
	W44804.1 GI:1328887	
	EST.	
	Homo sapiens (human)	
REFERENCE	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 242)	
	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,	
	Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,	
	Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,	
	Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and	
	Wilson,R.	
TITLE	The WashU-Merck EST Project	
	Unpublished (1995)	
	Contact: Wilson RK	
	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@watson.wustl.edu	
	This clone is available royalty-free through LLNL ; contact the	
	IMAGE Consortium (info@image.llnl.gov) for further information.	
FEATURES	Seq primer: mob.REGA+ET	
	High quality sequence stop: 233.	
	Location/Qualifiers	
	1..242	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="GDB:1258554"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:320896"	
	/tissue_type="parathyroid tumor"	
/dev_stage="adult"		
/lab_host="DH10B (ampicillin resistant)"		
source		
ORIGIN	Query Match	
	Best Local Similarity 81.8%; Pred. No. 5.1e-08; Length 591;	
	Matches 117; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	
	16 TTTTCTTTTGTGATGATTTTAATAAAATATCATTTCTTTTATTATTATTATTA	ACTT 75
	405 TATATATTGCTGCTTTTACATTTCTTTCTTTTAAATCTTATTATTATTA	ACTT 464
	76 TTAAGTTTATAGGTACATGTCGAAGTGTGCAGGTAGTACATATATACATG	TGCCA 135
	465 TTAAGTTTATAGGCACATGTGCACAAATGTCAGGTAGTACATATGTA	TATGTTGCCA 524
	136 TCGTGGTGTGCTGCACCCATTAA 158	
	525 TCGTGGTGTGCTGCACCCATTAA 547	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 78.1%; Pred. No. 5.9e-08; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 14.5%; Score 101.2; DB 10; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 14.5%; Score 101.2; DB 10; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 78.1%; Pred. No. 5.9e-08; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 14.5%; Score 101.2; DB 10; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
	University of Washington	
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
	Tel: (206) 616-3618	
	Fax: (206) 616-3887	
	Email: jwallace@u.washington.edu	
	Clones are derived from the human BAC library RPCI-11. For BAC	
	library availability, please contact Pieter de Jong	
COMMENT	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)	
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
	http://www.htsc.washington.edu	
	Plate: 983 row: M column: 24	
	Seq primer: T7	
	Class: BAC ends	
	High quality sequence stop: 527.	
	Location/Qualifiers	
FEATURES		
source		
ORIGIN	Query Match	
	Best Local Similarity 14.5%; Score 101.2; DB 10; Length 242;	
	Matches 121; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
	7 CACATAAGCTTTTTTTTTTGTGATGATTTTAATAAATATCATTTCTTTTATTATT	TTT 66
	54 CAGTAAGATTTTATTATTATTATTATTATTATTTCCTTTTAAATTTTATTATT	TTT 113
	67 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATA	TATA 126
	114 ATTATACCTTTTAAGCTTTTAGGTACATGTGCAATGTCAGGTAGTTACATATA	TATA 173
	127 CATGTGCCATGCTGCTGCTGCACCCATTAACTC 161	
	174 CATGTGCCATGCTGCTGCTGCACCAATTAACTC 208	
RESULT 14	AQ756779	
	LOCUS	
	DEFINITION	
	HS 5407 A2 G12 T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic_clone Plate=983 Col=24 Row=M, genomic survey sequence.	
	AQ756779	
	AQ756779.1 GI:5621498	
	GSS.	
	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 527)	
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,	
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	
	Hood,L.	
	Sequence-tagged connectors: A sequence approach to mapping and	
	scanning the human genome	
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL	10449764	
	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing	

```

source
1. .527
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=983 Col=24 Row=M"
/sex="male"
/clone_lib="pPCI-11 Human Male BAC Library"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 14.5%; Score 101.2; DB 11; Length 527;
Best Local Similarity 80.6%; Pred. No. 5.6e-08;
Matches 129; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGTACATTTTAATAAATATCATTTCTTTTTTTA 61
DB TTTTATNNTTATTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 132

QY 62 TTATTATATACCTTTTAAAGTTTTAGGTACATGTGCAAAAGTGCAGGTTAGTTACATAT 121
DB TTTTATTTTATATAC-TTTAAGTTTTAGGTACATGTGCACAAATGTGCAGGTTAGTTACATAT 191

QY 122 ATATACATGCGCATGCTGTGTGCTGCACCCCAATTAATC 161
DB TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 231

RESULT 15
CZ457195 445 bp DNA linear GSS 20-OCT-2005
LOCUS MCF740G11TR Human MCF7 breast cancer cell line library (MCF7_1)
DEFINITION Homo sapiens genomic clone MCF7_40_G11, genomic survey sequence.
ACCESSION CZ457195
VERSION CZ457195.1 GI:77933523
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS Volik,S.V., Raphael,B.J., Huang,G.-O., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
TITLE Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
tumor genome project
JOURNAL Unpublished (2005)
COMMENT Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
Location/Qualifiers
1. .445
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_40_G11"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library
(MCF7_1)"
/notes="Vector: pBACe3.1; Site_1: HindIII; This library was

```

```

ORIGIN
Query Match 14.4%; Score 100.8; DB 13; Length 445;
Best Local Similarity 76.9%; Pred. No. 6.7e-08;
Matches 123; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGTACATTTTAATAAATATCATTTCTTTTTTTA 61
DB TTTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 311

QY 62 TTATTATATACCTTTTAAAGTTTTAGGTACATGTGCARAGTGTGCAGGTTAGTTACATAT 121
DB TTTTATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 371

QY 122 ATATACATGCGCATGCTGTGTGCTGCACCCCAATTAATC 161
DB TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 411

RESULT 16
CR737970 746 bp mRNA linear EST 10-DEC-2004
LOCUS CR737970 Homo sapiens library (Ebert L) Homo sapiens cDNA clone
DEFINITION IMAGp998C11359 ; IMAGE:190402 5', mRNA sequence.
ACCESSION CR737970
VERSION CR737970.1 GI:51585934
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 746)
AUTHORS Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
Peters,M., Radelof,U. and Schneider,D.
TITLE I.M.A.G.E. cDNA Clone Collection
JOURNAL Unpublished (2004)
COMMENT Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: IMAGp998C11359.
RZPDLiB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAACAGCTATGAC.

FEATURES
Location/Qualifiers
1. .746
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998C11359 ; IMAGE:190402"
/clone_lib="Homo sapiens library (Ebert L)"

ORIGIN
Query Match 14.4%; Score 100.8; DB 8; Length 746;
Best Local Similarity 83.8%; Pred. No. 6.5e-08;
Matches 114; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 25 TTTTGATGATTTTAATAAATATCATTTCTTTTTTTTATTTATTTATTTTAAAGTTTT 84
DB TTTGGCCATTTTAAAGTAGTCTTTTTTTTAAATTTTATTTATTTATTTTAAAGTTTT 317

QY 85 AGGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTGTGT 144

```

constructed from MCF7 breast cancer cell line by Amplicon Express (<http://www.genomex.com>) using their standard procedure."

Db 318 AGGTTACATGCGCAACATGTCAGGTTTGTACATATGTATACATGTGCGCATGTTGGTGT 377
Qy 145 GCTGCACCCATTAACCT 160
Db 378 GCTGCACCCATTAACCT 393

RESULT 17
A0021610
LOCUS A0021610 417 bp DNA linear GSS 09-JUN-1998
DEFINITION CIT-HSP-2311P19.TR CIT-HSP Homo sapiens genomic clone 2311P19,
genomic survey sequence.
ACCESSION A0021610
VERSION A0021610.1 GI:3200346
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 417)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2311P19.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
FEATURES
source
1..417
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clones="2311P19"
/sex="Male"
/cell_type="Sperm"
/clone_libs="CIT-HSP"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
Query Match 14.4%; Score 100.6; DB 11; Length 417;
Best Local Similarity 81.1%; Pred. No. 7.3e-08;
Matches 129; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
Qy 2 TGTTTCACATAAAGTTTTTTTTTTTGATGATTTTATAAATAATCATCTTTCTTTTATA 61
Db 103 TTTTTCCTATTGATCTTCATCTTTTTTTTTTTCTTTTATTATTATTATTATTATTA 162
Qy 62 TTATTATTATCTTTTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATAT 121
Db 163 TTATTATTATAC-TTTAAGTTTATAGGGTACATGTGCAACATGTGCAGGTAGTTACATAT 221
Qy 122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACT 160
Db 222 GTATACATGTGCCATGCTGGTGTGCTGCACCCACTAACT 260

RESULT 18
CB048927/c

LOCUS CB048927 225 bp mRNA linear EST 17-JAN-2003
DEFINITION NISC_g107f10.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271074
5', mRNA sequence.
ACCESSION CB048927
VERSION CB048927.1 GI:27787214
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 225)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: L1AM8007 row: L column: 19
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
FEATURES
source
1..225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:3271074"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA
from the normalized library NCI CGAP Pr22 was prepared,
and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 985608-986759, 1101192-1101959, and
1217928-1220615). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN

Query Match 14.3%; Score 100.4; DB 4; Length 225;
Best Local Similarity 84.9%; Pred. No. 8.1e-08;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 16 TTTTCTTTTGTGATGATTTTATAAATAATCATCTTTCTTTTATTATTATTATATACTT 75
Db 170 TTTTCTTTTGTGATGATTTTATAAATAATCATCTTTCTTTTATTATTATTATATACT 112
Qy 76 TTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGCGCA 135
Db 111 TTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATGATGATGCGCA 52
Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db 51 TGCTGGTGTGCTGCACCCACTAACTC 26

RESULT 19
CB410332/c
LOCUS CB410332 233 bp mRNA linear EST 24-MAR-2003
DEFINITION NISC_nc11a06.y1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776426
5', mRNA sequence.
ACCESSION CB410332
VERSION CB410332.1 GI:29167072
KEYWORDS EST.

Qy 2 TGTTTACATGAAGTTTTTTTTTTTGTGATGATTTTAATAAAATATCAATTTCTTTTTTTA 61
 Db 352 TGCTCAGCTTGAAGAACTTAATATGAATTTCTTTTTTTTCTTTTTTATATATATTA 411
 Qy 62 TTATTTATTTACTTTTAAAGTTTTTTAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATAT 121
 Db 412 TTATTTACTATACTTTTAAAGTTTTTTAGGTACATGTCGACATTTCTGCAGGTTAGTTACATAT 471
 Qy 122 ATATACATGTGCATGCTGGTGTGCTGCACCCCACTAACTCA 162
 Db 472 GTATACATGTGCCATGCTGGTGGCTGCACCCCACTAACTCA 512

RESULT 26
 C2450878 870 bp DNA linear GSS 20-OCT-2005
 LOCUS MCF731m05TF Human MCF7 breast cancer cell line library (MCF7_1)
 DEFINITION Homo sapiens genomic clone MCF7_31m05, genomic survey sequence.
 ACCESSION C2450878
 VERSION C2450878.1 GI:77927140
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Volik S.V., Raphael B.J., Huang G.-Q., Murnane J., Brebner J.H., Bajsarowicz K., Paris P., Tao Q., Kowbel D., Lapuk A.V., Kuo W.-L., Shagin D.A., Shagina I.A., Magrane G., Gray J.W., Jan F.-C., de Jong P., Pevzner P. and Collins C.
 Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
 Unpublished (2005)
 JOURNAL Contact: Volik Sv
 COMMENT Colin Collins' lab
 UCSF Comprehensive Cancer Center
 UCSF Box 0808, San Francisco, CA 94143-0808, USA
 Tel: 415 502 7066
 Fax: 415 502 5665
 Email: svolik@cc.ucsf.edu
 This clone is available from Amplicon Express
 http://www.genomex.com
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..870
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="MCF7_31m05"
 /sex="female"
 /clone_lib="Human MCF7 breast cancer cell line library (MCF7_1)"
 /note="Vector: pCEBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN
 Query Match 14.3%; Score 100.2; DB 13; Length 870;
 Best Local Similarity 76.4%; Pred. No. 8.2e-08;
 Matches 123; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 CTGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAAATATCAATTTCTTTTTTT 60
 Db 156 CTCCTTCTTATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 215
 Qy 61 ATTATTTATTTACTTTTAAAGTTTTTTAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATA 120
 Db 216 ATTTTATTTATTTACTTTTAAAGTTTTTTAGGTACATGTCGACATTTCTGCAGGTTAGTTACATA 275
 Qy 121 TATATACATGTGCCATGCTGGTGTGCTGCACCCCACTAACTC 161

Db 276 TGATATACATGTGCCATGCTGGTGTGCTGCACCCCACTAACTC 316

RESULT 27
 AA344409 307 bp mRNA linear EST 21-APR-1997
 LOCUS EST50301 Gall bladder I Homo sapiens cDNA 5' end similar to EST
 DEFINITION containing L1 repeat, mRNA sequence.
 ACCESSION AA344409
 VERSION AA344409.1 GI:19986648
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Adams M.D., Lee N.H., Kirkness E.F., Weinstock K.G., Gocayne J.D., Bult C.J., Sutton G., Blake J.A., Brandon R.C., Man-Wai C., White O., Sutton G., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D., Claydon R.A., Clifton W.M., Fritchman J.L., Geoghegan N.S., Fitzgerald L.M., Fitzhugh W.M., Hanna M.C., Hedblom E., Hinkle P.S., Jr., Glodek A., Gnehm C.L., Li L.-I., Marmaros S.M., Merrick J.M., Kelley J.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palacios R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li F., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J., Dimke D., Feng D.-F., Ferrie A., Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K., Kozak D.L., Kunsch C., Hungjun J., Li H., Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.M., Dillion P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 7566098
 Other_ESTs: THC145780
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source Location/Qualifiers
 1..307
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):145948"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="adult, 25 yrs"
 /clone_lib="Gall bladder I"
 /note="Organ: gall bladder; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Query Match 14.3%; Score 100; DB 1; Length 307;
 Best Local Similarity 80.6%; Pred. No. 9.4e-08;
 Matches 129; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 2 TGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAAATATCAATTTCTTTTTTTA 61
 Db 240 TAATTTATTTATTTTATTTATTTTGTGGTGGTCTTCTTATGAAGTTTCTTTCTTTATTA 181
 Qy 62 TTATTTATTTACTTTTAAAGTTTTTTAGGTACATGTCGCAAGTGTGCAGGTTAGTTACATAT 121

[illegible]

RESULT_30	AL601657	677 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	AL601657				
DEFINITION	DKF2P313M126.r1.313 (synonym: hlcc2) Homo sapiens cDNA clone DKF2P313M126-5', mRNA sequence.				
ACCESSION	AL601657				
VERSION	AL601657.2	GI:34476508			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 677)				
AUTHORS	Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.				
TITLE	EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., et al.)				
JOURNAL	Unpublished (2003)				
COMMENT	On Aug 10, 2001 this sequence version replaced gi:15165163. Contact: MIPS				

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp313M126) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

```

FEATURES
    source
        Location/Qualifiers
            1..677
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFP313M126"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="313 (synonym: hlcc2)"
                /note="vector: pTriplex2; Site_1: SfiI; Site_2: SfiIB;
                cDNA-collection"

```

Query Match 14.3%; Score 100; DB 1; Length 677;

	Best Local Similarity	80.6%	Pred. No. 9e-08;	Mismatches	Indels	Gaps
	Matches	Conservative	0;	30;	1;	1
QY	2	TGTTTCACATAAAGT	TTTTTTTTTGATGAATTTTAATAAAATATCAT	TTCTTTTTTTTA	61	
Dd	37	TGTTTGTGTTTTGGTTTTTTT	TTTTTGTGTTTTTGTGTTTTTGTGTTTTTAAATTA	TTA	96	
QY	62	TTATTATTATACT	TTTTTAAGTTTAGGGTACATGTGC	AAGTGTGCAGGTAGTTACATAT	121	
Dd	97	TTATTATTATAC-	TTTAAAGTTTTAGGGTACATGTGC	CAATGTGCAGGTAGTTACATAT	155	
QY	122	ATATACATGCCCATCGTGGTGTGCTGCACC	CCTAAC	TCTC	161	
Dd	156	GTATACATGCCCATCGTGGTGTGCTGCACC	CCTAAC	TCTC	195	

RESULT	31
AQ266524	
LOCUS	
DEFINITION	AQ266524 272 bp DNA linear
	RPCI11-75A2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-75A2,
	genomic survey sequence.
ACCESSION	AQ266524
VERSION	AQ266524.1 GI:3794128
KEYWORDS	GSS.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 272) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE	Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other GSSs: RPC111-75A2.TJ Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208

Email: mcdams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (inforesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

```

FEATURES
source
Class: BAC end.
Location/Qualifiers
1. 272
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7528417"
/db_xref="taxon:9606"
/clone="RPC1-11-75A2"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6;
RPC111 Human Male BAC Li

```

Query Match	14.2%	Score 99.6;	DB 11;	Length 272;
Best Local Similarity	81.0%;	Pred. No. 1.1e-07;		
Matches 128; Conservative	0;	Mismatches 29;	Indels 1;	Gaps 1;
Qy	4	TTTCACATAAAGTTTTTTTTTTTTTGATGATTAAATAAAAATACATTTTCTTTTTTTATT	63	
Dd	82	TTCGTCTTCACATTCCTTTTTTTTTTGCAGGTTTTTAATTTATTTATTTATTTTCATT	141	
Qv	64	ATTATTATATCTTTTAAGTTTTTAGGGTACAATGTCGAAGTGTGCAAGGTTAGTTACATATAT	123	

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homniidae; Eutheria; Euarchontoglires; Primates; Catarrhini;
1 (bases 1 to 548)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Title Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPC11-20K18-TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..548
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7507553"
/db_xref="taxon:9606"
/clone="RPCI-11-20K18"
/sex="Male"
/cell_type="Lymphocytes"
/clone_libs="RPCI-11"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN
Query Match 14.2%; Score 99.4; DB 11; Length 548;
Best Local Similarity 77.1%; Pred. No. 1.2e-07;
Matches 121; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 5 TTCACATAAAGCTTTTCTTTTGGATGATTTTAATAAATATCATTTCTTTTATTATA 64
Db 286 TTCACATTTCTTTTCTTTTAAAGTGTGTAACCCCTAGAATTTGTTTGTGTTTTT 345
Qy 65 TTATTATACCTTTTAAGTTTAAAGGTGACATGTGCAAGTGTGCAGTTAGTTACATATA 124
Db 346 TTAATTATACCTTTTAAGTTTAAAGGTGACATGTGCAAGTGTGTTTACATATA 405
Qy 125 TACATGTGCCATGCTGGTGTCTGCACCCATTAACTC 161
Db 406 TACATGTGCCATGTTGGTGTCTGCACCCATTAAAC 442

RESULT 35
BQ007697
LOCUS
DEFINITION UI-H-E10-ayh-c-22-0-UI-s1 NCI CGAP_E10 Homo sapiens cDNA clone
IMAGE:5838669 3', mRNA sequence.
ACCESSION BQ007697
VERSION BQ007697.1 GI:19732597
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE 1 (bases 1 to 771)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 2-54, >(TAAA)n#Simple repeat (matched complement) 57-287,
>L1P2#LINE/L1 (matched complement)
Seq primer: M13 FORWARD
POLyA=yes.

FEATURES
source Location/Qualifiers
1..771
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5838669"
/tissue type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP E10"
/note="Organ: Left Pelvis; Vector: p77T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoRI; Site 2: Not I;
NCI CGAP E10 is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoRI adaptor, digested
with Not I, and cloned directionally into p77T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is ACACCTTGCAC.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-E10
TAG_SEQ=ACACTTGCAC"

ORIGIN
Query Match 14.2%; Score 99.4; DB 3; Length 771;
Best Local Similarity 84.8%; Pred. No. 1.1e-07;
Matches 123; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 16 TTTTCTTTTCTTGGATGATTTTAAATAATATCATTTCTTTTCTTTTATTATTATTA 75
Db 8 TTTTCTTTTCTTGGATGATTTTAAATAATATCATTTCTTTTCTTTTATTATTATTA 66
Qy 76 TTAAGTTTAAAGGTGACATGTGCAAGTGTGCAGTTAGTTACATATATACATGTGCCA 135
Db 67 TTAAGTTCTAGGTGACATGTGCAACATGCAGTTTGTGTACATATGTATACATGTGCCA 126
Qy 136 TGCTGGTGTCTGCACCCATTAACT 160
Db 127 TGTGTGTGTCTGCACCCATTAACT 151

RESULT 36
BQ924499/c
LOCUS
DEFINITION BQ924499 8882064 lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6198008 5', mRNA sequence.
ACCESSION BQ924499
VERSION BQ924499.1 GI:22339530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 906)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13608 row: p column: 09

High quality sequence stop: 554.

Location/Qualifiers

1..906

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6198008"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

/lab_host="DH10B"

/clone_lib="Lupski sciatic nerve"

/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:

NotI; Site 2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACCGCTCG-3' and

5'-GACTAGTCTAGACGCGAGCGGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.87 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

ORIGIN

Query Match 14.2%; Score 99.4; DB 3; Length 906;

Best Local Similarity 77.1%; Pred. No. 1.1e-07;

Matches 121; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 6 TCACATAAAGTCTTTTCTTTTGTGATGATTTAATAAATATCATCTTTCTTTTATTAT 65

Db 207 TCAATAAAGCATGACCTTCCTTGGAACTTGCTCTTTCTTTTCTTTTCTTTT 148

Qy 66 TATTATATCTTTTAAAGTTTAAAGGTACATGTGCAAGTGCAGGTAGTTACATATAT 125

Db 147 AATTATATCTTTTAAAGTTCTAGGTACATGTGCAATGTGCAGTTTGTACGTATGAT 88

Qy 126 ACATGTGCCATGCTGTGTGCTGCACCCATTAACATCA 162

Db 87 ACATGTGCCATGTGGTTTGGTCTGCACCCATTAACATCA 51

RESULT 37

AQ319769

LOCUS

AQ319769 571 bp DNA linear GSS 06-MAY-1999

DEFINITION

RPC111-10717-TV RPC111 Homo sapiens genomic clone RPC111-10717,

genomic survey sequence.

ACCESSION

AQ319769

VERSION

AQ319769.1 GI:4052657

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 571)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,

Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building

TITLE

JOURNAL

COMMENT

Unpublished (1998)

Other_GSSs: RPC111-10717.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@igr.org

Clones are derived from the human BAC library RPC111. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..571

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7540902"

/db_xref="taxon:9606"

/clone="RPC111-10717"

/sex="Male"

/cell_type="Lymphocytes"

/clone_lib="RPC111"

/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;

RPC111 Human Male BAC Library"

ORIGIN

Query Match

Best Local Similarity

Matches 130;

Conservative

0;

Mismatches

33;

Indels

1;

Gaps

1;

Qy

20

TTTTTTTTCATGATTTTAATAAAATATCATCTTTCTTTTATTATTATTATATATTTAA 79

Db

246

TTGATATTTGTTTGTGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAA 304

Qy

80

GTTTTAGGTACATGTCACCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATGCT 139

Db

305

GTTTTAGGTACATGTCACCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATGCT 364

Qy

140

GGTGTCTCCACCCCACTCATCTTTTAAATTT 183

Db

365

GGTGTCTCCACCCCACTCATCTTTAGCATAGGTATATCT 408

RESULT 38

LOCUS

AQ446110

DEFINITION

z66003.s1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone

IMAGE:774413 3' similar to gb:L19872 AH RECEPTOR PRECURSOR

(HUMAN); contains L1.b2 L1 repetitive element ;, mRNA sequence.

ACCESSION

AA446110

VERSION

AA446110.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 401)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,

Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wyllie,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: es@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m3 fwd. ET from Amersham

High quality sequence stop: 369.

FEATURES

source

Location/Qualifiers

1..401
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:774413"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares total fetus Nb2HF9 9w"
 /note="Vector: pT73D-PaCI; Site_1: Not I; Site_2: Eco RI;
 1st strand cDNA was prepared from mRNA obtained from
 pooled 8-9 week (total) fetus material with a Not I -
 oligo(dT) primer [5',
 TGTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 14.1%; Score 99; DB 1; Length 401;
 Best Local Similarity 86.5%; Pred. No. 1.4e-07;
 Matches 122; Conservative 0; Mismatches 15; Indels 4; Gaps 1;
 Qy 21 TTTTTCATGATTTTAATAAAATATCATTTTCTTTTATTTATTTATTTATTTAAAG 80
 Db 1 TTTTTCGAGAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAAAG 56
 Qy 81 TTTTAGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATGCTG 140
 Db 57 TTTTAGGTACATGTGCAATGTGCAGTTAGTTACATATATATACATGTGCCATGCTG 116
 Qy 141 GTGTGTCACCCATTAACTC 161
 Db 117 GTGTGCGCCACCCATTAACTC 137

RESULT 39
 LOCUS A0029723
 DEFINITION RPC111-41N20.TV RPCI-11 Homo sapiens genomic clone RPCI-11-41N20,
 genomic survey sequence.
 ACCESSION A0029723
 VERSION A0029723.1 GI:3274854
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
 Venter,J.C.
 TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mcadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..464
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7515691"
 /db_xref="taxon:9606"
 /clone="RPCI-11-41N20"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACes.6; Site_1: EcoRI; Site_2: EcoRI;
 RPC111 Human Male BAC Library"

ORIGIN

Query Match 14.1%; Score 99; DB 11; Length 464;
 Best Local Similarity 82.0%; Pred. No. 1.4e-07;
 Matches 114; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 Qy 23 TTTTTCATGATTTTAATAAAATATCATTTTCTTTTATTTATTTATTTATTTAAAGTT 82
 Db 81 TTTTTCGTGCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 140
 Qy 83 TTAGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATGCTCGT 142
 Db 141 TTAGGTACATGTGCACATTTGTCAGTTAGTTACATATGTATATATGTGCCATGCTCGT 200
 Qy 143 GTGTGTCACCCATTAACTC 161
 Db 201 GCGCTGCACCCACTAACTC 219

RESULT 40
 LOCUS DB302517/c
 DEFINITION DB302517 BRAWY2 Homo sapiens cDNA clone BRAWY2030702 3', mRNA
 sequence.
 ACCESSION DB302517
 VERSION DB302517.1 GI:83085415
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 553)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
 Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
 Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
 Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification and Characterization of Putative Alternative
 Idenification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

```

FEATURES
source
1...553
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2030702"
/tissue_type="amygdala"
/clone_lib="BRAMY2"
/notes="Vector, mvec16SF13"

```

Query Match	14.1%	Score 99	DB 9	Length 553
Best Local Similarity	85.3%	Pred. No.	1.4e-07	
Matches 122	Conservative	0	Mismatches 20	Indels 1
				Gaps 1

Qy	19 TTTTTTTTGGACATTTTAATAAAATATCATTTTCCTTTTTATTATTATTACTTTTA 78
Db	518 TATATTCCCTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATAC-TTTA 460

Qy	79	AGTTTTAGGGTACATGTCGAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGC	138
Db	459	AGTTTTAGGGTACATGTCGACAGTGTGCAGGTTAGTTACATATGTATACATGTGCCATGC	400

Oy		139	TGCTGTCTGCACCCATTAACTC	161
Dδ		399	TGCTGTCTGCACCCATTAACTC	377

RESULT 41
AG042325
LOCUS
AG042325
665 bp
DNA
linear
GSS 01-NOV-2001
DEFINITION
Pan troglodytes DNA, clone: PTB-020E21.F, genomic survey sequence.

ACCESSION AG042325
VERSION AG042325.1 GI:16571050
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Fungi, Cryptogametes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominiidae; Pan.

1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe H. and Sakaki, Y. BAC end sequences of Library PTB
REFERENCE	
AUTHORS	
TITLE	

JOURNAL
REFERENCE
AUTHORS

TITLE
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suebi-cho, Wako, Saitama, Japan
230-0045

CLONE	COMMENT
<p>(E-mail: chimbee@gsc.riken.go.jp, URL: http://hgpc.gsc.riken.go.jp/; Tel: 81-45-503-9111, Fax: 81-45-503-9170)</p>	<p>This BAC end was cloned from the chimpanzee BAC library PTB. This BAC end was used for the identification of the chimpanzee BAC library.</p>

```

clone tracking errors.
PRIMERS
Sequencing: -21M13
+-----

```

```

Vector      : pks145
R.Site 1   : Sac1
R.Site 2   : Sac1
Vector      : pks145
R.Site 1   : Sac1
R.Site 2   : Sac1

```

```
source
1..685
/organism="Pan troglodytes"
/mol_type="genomic DNA"
```

```

/clone="PTB-020E21.F"
/sex="male"
/cell_type="lymphoblast"

```

```
/clone lib="PTB Chimpanzee Male BAC Library"
```

Query Match	14.1%	Score 99	DB 14	Length 665
Best Local Similarity	85.3%	Pred. No. 1.4e-07		
Matches 122	Conservative	0	Mismatches 20	Indels 1
				Caps 1

Qy	19	T T T T T T T T G A T G A T T T T A A G A A A A T A C A T T T C T T T T T T T T A T T A T T A T A T A C T T T T A	78
Db	294	T T T T T T T T C T T T T T T T T A T T A T T A T T A T T A T T A T T A T T A T T A T A C - T T T A	352

Qy	79	AGTTTTAGGGTACATGTCAAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGC	138
Dh	353	AGTTTTAGGGTACATGTCGCAATATGTCAGGTAGTTACCTATGTTATACATGTGCCATGC	412

Qy	139	TGGTGTGCTGCACCCATTAACTC	161
Dh	413	TGGTGGCTGCACCCACCTAACTC	435

RESULT	42
AQ779743	
LOCUS	AQ779743
DEFINITION	HS_5571_B2_H10.SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1147 Col=20 Row=P, genomic survey sequence.
	704 bp DNA linear GSS 02-AUG-1999

ACCESSION
VERSION
Q779743.1 GI:5682703
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)

ORGANISM

REFERENCES
 I. J. BASS, *J. CO. 704*
 Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,
 Kellier, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and
 Hood, L.

JOURNAL
sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
104349764
TURNED

CONTACT: MANARIAS GJ, WALLACE JC, HOOD L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North Seattle, WA 98109. USA

rel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11 For BAC

library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm).
 OAC from Recombinant Genetics (info@recom.com). BAC and Web-Server.

http://www.htsc.washington.edu
 Plate: 1147 row: P column: 20
 Seq primer: SP6
 ori

FEATURES
source
Location/Qualifiers
1..704
High quality sequence stop: 704.

```

/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=1147 Col=20 Row=p"

```

/clone lib="RPCI-11 Human Mac BAC Library"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
Male blood DNA was isolated from one randomly chosen donor"

ORIGIN

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini, Homidae; Homo.

REFERENCE 1 (bases 1 to 424)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

JOURNAL Unpublished (1998)

COMMENT Other GSSs: CIT-HSP-2328018.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES

Location/Qualifiers

1..424

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="2328018"

/sex="Male"

/cell_type="Sperm"

/clone_lib="CIT-HSP"

/notes="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 14.1%; Score 98.8; DB 11; Length 424;

Best Local Similarity 79.6%; Pred. No. 1.5e-07;

Matches 129; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 1 CTGTTTTCACATAAGTTTCTTTTCTTTTGTATGATTTTATAAAATATCATCTTTCTTTT 60

|||||

Db 298 CTGAGCCAAGAAGATAAGCCTTTTAAATTATTTATTTATTTATTTATTT 239

QY 61 ATTATTATTATACATTTTAAAGTTTATAGGTACATGTGCACAAAGTGTGCAGTTAGTTACATA 120

|||||

Db 238 ATTATTATTATACATTTTAAAGTTTATAGGTACATGTGCACAAAGTGTGCAGTTAGTTACATA 180

QY 121 TATATACATGTCCATGCTGTTGCTGCACCCATAACTCA 162

|||||

Db 179 TGTATACATGTCCATGCTGTTGCTGCACCCATAACTCA 138

RESULT 45

AQ127855

LOCUS HS_3094_Al_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3094 Col=3 Row=C, genomic survey sequence.

DEFINITION

ACCESSION AQ127855.1 GI:3505021

VERSION AQ127855

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 468)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3094 row: C column: 3
 Class: BAC ends
 High quality sequence stop: 468.
 Location/Qualifiers
 1. .468
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3094 Col=3 Row=C"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
 Query Match 14.1%; Score 98.8; DB 11; Length 468;
 Best Local Similarity 78.7%; Pred. No. 1.5e-07;
 Matches 118; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 11 TAAAGTTTTTTTTTTGATGATTTAAATAAATATCATTTCTTTTATTTATTTATTA 70
 Db 95 TATTTTTTATTTATTTTATTTTCAATATTTTATTTATTTATTTATTTATTTATTT 154
 QY 71 TACTTTTAAAGTTTGGGTACATGTCGAAGTGTGAGTGTAGTTCATATATATACATG 130
 Db 155 ATACTTTAAAGTTTGGGTACATGTCGAAGTGTGAGTGTAGTTCATATATACATG 214
 QY 131 TGGCATGCTGGTGTGCTGCCACCACTAACT 160
 Db 215 TGACATGCTGGTGTGCTGCCACCACTAACT 244

RESULT 46
 AQ550918/c
 LOCUS
 DEFINITION RPCI-11-383F14.TV RPCI-11 Homo sapiens genomic clone
 RPCI-11-383F14, genomic survey sequence.
 ACCESSION AQ550918
 VERSION AQ550918.1 GI:4910095
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 561)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-383F14.TJ
 CONTACT: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC

Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3094 row: C column: 3
 Class: BAC ends
 High quality sequence stop: 468.
 Location/Qualifiers
 1. .561
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3094 Col=3 Row=C"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
 Query Match 14.1%; Score 98.8; DB 11; Length 561;
 Best Local Similarity 76.6%; Pred. No. 1.5e-07;
 Matches 121; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 4 TTTCATATAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTATTTAT 63
 Db 479 TTAGCTGTGCATGTTCTTTTCTTTTATTTATTTATTTATTTATTTATTTATTTAT 420
 QY 64 ATTATTATATCTTTTAAGTTTTTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATAT 123
 Db 419 TATTATTATACTTTAAAGTTTTTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATGT 360
 QY 124 ATACATGTGCCATGCTGGTGTGCTGCCACCACTAACT 161
 Db 359 ATACATGTGCCATGCTGGTGTGCTGCCACCACTAACT 322

RESULT 47
 BQ447264
 LOCUS
 DEFINITION UI-H-EU1-bad-1-23-0-UI.s1 NCI CGAP Ctl Homo sapiens cDNA clone
 UI-H-EU1-bad-1-23-0-UI 3', mRNA sequence.
 ACCESSION BQ447264
 VERSION BQ447264.1 GI:21250376
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 725)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 1-48, >(TAAA)n#Simple repeat (matched complement) 51-169, >L1PA2#LINE/L1 (matched complement) 413-454,
 >AT rich#Low complexity 498-590, >MIR#SINE/MIR (matched complement)
 Seq primer: M13 FORWARD
 POLYA=tes.

FEATURES
 source
 Location/Qualifiers
 1. .725
 /organism="Homo sapiens"

library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (inforesgen.com). BAC end search page: http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1. .561
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RPCI-11-383F14"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN
 Query Match 14.1%; Score 98.8; DB 11; Length 561;
 Best Local Similarity 76.6%; Pred. No. 1.5e-07;
 Matches 121; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 4 TTTCATATAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTATTTAT 63
 Db 479 TTAGCTGTGCATGTTCTTTTCTTTTATTTATTTATTTATTTATTTATTTATTTATTT 420
 QY 64 ATTATTATATCTTTTAAGTTTTTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATAT 123
 Db 419 TATTATTATACTTTAAAGTTTTTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATGT 360
 QY 124 ATACATGTGCCATGCTGGTGTGCTGCCACCACTAACT 161
 Db 359 ATACATGTGCCATGCTGGTGTGCTGCCACCACTAACT 322

RESULT 47
 BQ447264
 LOCUS
 DEFINITION UI-H-EU1-bad-1-23-0-UI.s1 NCI CGAP Ctl Homo sapiens cDNA clone
 UI-H-EU1-bad-1-23-0-UI 3', mRNA sequence.
 ACCESSION BQ447264
 VERSION BQ447264.1 GI:21250376
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 725)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 1-48, >(TAAA)n#Simple repeat (matched complement) 51-169, >L1PA2#LINE/L1 (matched complement) 413-454,
 >AT rich#Low complexity 498-590, >MIR#SINE/MIR (matched complement)
 Seq primer: M13 FORWARD
 POLYA=tes.

FEATURES
 source
 Location/Qualifiers
 1. .725
 /organism="Homo sapiens"


```
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="UI-H-EU1-bad-1-23-0-UI"  
/tissue_type="Osteoarthritic Cartilage"  
/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_lib="NCI CGAP Ctl"  
/note="Organ: Knee; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP Ctl is a normalized cDNA library containing the  
following tissue(s): Osteoarthritic Cartilage The library  
was constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
TGATCACGCT.  
TAG_TISSUE=osteoarthritic cartilage  
TAG_LIB=UI-H-EU1  
TAG_SEQ=TGATCACGCT"
```

ORIGIN

```
Query Match 14.1%; Score 98.8; DB 3; Length 725;  
Best Local Similarity 84.2%; Pred. No. 1.5e-07;  
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
  
Qy 16 TTTTCTTTTGGATGATTTAATAAAATATCAATTTCTTTTATTATTATTACTT 75  
|||||  
Db 2 TTTTCTTTTGGATGATTTAATAAAATATCAATTTCTTTTATTATTATTACTT 60  
|||||  
  
Qy 76 TTAAGTTTGTAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 135  
|||||  
Db 61 TTAAGTTTGTAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 120  
|||||  
  
Qy 136 TGCTGGTGTGCTGCACCCATTAACCTC 161  
|||||  
Db 121 TGCTGGTGTGCTGCACCCATTAACCTC 146  
|||||
```

```
RESULT 48  
BC032464/c  
LOCUS  
DEFINITION MCF725h15TF Human MCF7 breast cancer cell line library (MCF7_1)  
ACCESSION BC032464  
VERSION BC032464.1 GI:77922503  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 853)  
Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,  
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,  
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de  
Jong,P., Pevzner,P. and Collins,C.  
Decoding the genomic architecture and high throughput detection of  
fusion transcripts in breast cancer cell lines: Implications for a  
tumor genome project  
Unpublished (2005)  
Contact: Volik SV  
Colin Collins' lab  
UCSF Comprehensive Cancer Center  
UCSF Box 0808, San Francisco, CA 94143-0808, USA  
Tel: 415 502 7066  
Fax: 415 502 5665  
Email: svolik@cc.ucsf.edu  
This clone is available from Amplicon Express
```

```
http://www.genomex.com  
Class: BAC ends.  
Location/Qualifiers  
source 1..853  
/organism="Homo sapiens"  
/mol_type="genomic DNA"  
/db_xref="taxon:9606"  
/clone="MCF7_25h15"  
/sex="female"  
/clone_lib="Human MCF7 breast cancer cell line library  
(MCF7_1)"  
/note="Vector: pECBAC1; Site 1: HindIII; This library was  
constructed from MCF7 breast cancer cell line by Amplicon  
Express (http://www.genomex.com) using their standard  
procedure."
```

ORIGIN

```
Query Match 14.1%; Score 98.8; DB 13; Length 853;  
Best Local Similarity 84.2%; Pred. No. 1.5e-07;  
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
  
Qy 16 TTTTCTTTTGGATGATTTAATAAAATATCAATTTCTTTTATTATTATTACTT 75  
|||||  
Db 228 TTTTCTTTTGGATGATTTAATAAAATATCAATTTCTTTTATTATTATTACTT 169  
|||||  
  
Qy 76 TTAAGTTTGTAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 135  
|||||  
Db 168 -TTAAGTTTGTAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 110  
|||||  
  
Qy 136 TGCTGGTGTGCTGCACCCATTAACCTC 161  
|||||  
Db 109 TGCTGGTGTGCTGCACCCATTAACCTC 84  
|||||
```

```
RESULT 49  
BC032464/c  
LOCUS  
DEFINITION Homo sapiens, clone IMAGE:5210997, mRNA.  
ACCESSION BC032464  
VERSION BC032464.1 GI:22749645  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 3088)  
Strausberg,R.  
Direct Submission  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
Sequencing Center by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc_mgc@nhgri.nih.gov
```

```
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
Sequencing Center by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc_mgc@nhgri.nih.gov
```

```
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
Sequencing Center by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc_mgc@nhgri.nih.gov
```

```
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
Sequencing Center by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc_mgc@nhgri.nih.gov
```

```
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
Sequencing Center by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc_mgc@nhgri.nih.gov
```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 64 Row: j Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: frame shifted.

FEATURES

source
1. .3088
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5210997"
/tissue_type="Blood, adult leukocytes"
/clone_lib="NIH_MGC_118"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 14.1%; Score 98.8; DB 6; Length 3088;
Best Local Similarity 84.2%; Pred. No. 1.4e-07;
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATTTTAAATAAATATATCTTTCTTTTATTTATTTATTTACTT 75
|||||
Db 3063 TTTTCTTTTTCATGATTTTAAATAAATATATCTTTCTTTTATTTATTTATTTACTT 75
|||||

QY 76 TTAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGCGCCA 135
|||||
Db 3004 TTAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGCGCCA 2945
|||||

QY 136 TGTCTGTGTCTGCACCCATTAATCT 161
|||||
Db 2944 TGTCTGTGTCTGCACCCATTAATCT 2919
|||||

RESULT 50

AQ017761
LOCUS
DEFINITION
CIT-HSP-2304A13.TR CIT-HSP Homo sapiens genomic clone 2304A13,
genomic survey sequence.

ACCESSION

AQ017761

VERSION

AQ017761.1 GI:3196497

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 324)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1998)
Other_GSSs: CIT-HSP-2304A13.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source

1. .324

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"
/clone="2304A13"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN

Query Match 14.1%; Score 98.4; DB 11; Length 324;
Best Local Similarity 79.1%; Pred. No. 1.8e-07;
Matches 117; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 12 AAAGTTTTTTTTTTTGATGATTTTAAATAAATATATCATTTTCTTTTATTTATTTAT 71
|||||
Db 142 AAAATTAA 201
|||||

QY 72 ACTTTTAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGT 131
|||||
Db 202 TACTCTAAGTTTTCAGGTACATGTGCACATTTGGCAGGTAGTTACATATATATACATGT 261
|||||

QY 132 GCATGCTGCTGCTGCACCCATTAAC 159
|||||
Db 262 GCATGCTGCTGCTGCCTGTACCCACTAAC 289
|||||

RESULT 51

AQ605001

LOCUS

DEFINITION

HS 2119 B1 A12 T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2119 Col=23 Row=B, genomic survey
sequence.

ACCESSION

AQ605001

VERSION

AQ605001.1 GI:5064995

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 398)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: iwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2119 row: B column: 23
Seq primer: T7
Class: BAC ends
High quality sequence stop: 398.
Location/Qualifiers
1. .398

FEATURES

source

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=2119 Col=23 Row=B"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match	14.18	Score 98.4	DB 11	Length 398
Best Local Similarity	79.1%	Pred. No. 1.8e-07		
Matches 117	Conservative 0	Mismatches 31	Indels 0	Gaps 0
QY	14	AGTTTTTTTTTGGATGATTTTTAATAAAATATCATTTCTCTTTTTTATTATTATTATAC	73	
Db	164	AGCATTTTTCGTTGCTGTTGTTTTGTTTTGTTTTCTTTTTTTTATTATTATAC	223	
QY	74	TTTTAAAGTTTTAGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATATACATGTGC	133	
Db	224	TTTTAAAGTTTTAGGGTACATGTGCACATGTGCAGGTTAGTTACATATGATATACATGTGC	283	
QY	134	CATGCTGGTGTGCTGCACCCCAATTAACTC	161	
Db	284	CATGCTGGTGTGCTGCACCCCACTAACTC	311	

```

RESULT 52
BX115372
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

BX115372 713 bp mRNA linear EST 07-FEB-2003
BX115372 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE999M18117 ; IMAGE:123065, mRNA sequence.
BX115372
BX115372.1 GI:27939389
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 713)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolf
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE999M18117.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi?responsefileNo=972 Contact: Ina Rolf
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.

```

```

FEATURES
source
Location/Qualifiers
1. .713
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:998M18117 ; IMAGE:123065"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACCTGGAGAACTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. "
```

ORIGIN

Query Match

14.1%; Score 98.4; DB 4; Length 713;

[illegible]

RESULT 53	BU607283	LOCUS	273 bp	linear	EST 21-FEB-2003
DEFINITION	UI-CF-FNO-aeu-e-07-0-UI.s1	UI-CF-FNO Homo sapiens cDNA clone			
ACCESSION	BU607283	UI-CF-FNO-aeu-e-07-0-UI 3', mRNA sequence.			
KEYWORDS	BU607283.1	GI:23270558			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
AUTHORS	Ekukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 273)				
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.				
JOURNAL	Normalization and subtraction: two approaches to facilitate gene				
PUBMED	Genome Res. 6 (9), 791-806 (1996)				
COMMENT	8889548				
	Contact: McCray, PB				
	McCray Lab				
	University of Iowa				
	2024 University of Iowa Med Labs, Iowa City, IA 52242, USA				
	Tel: 319 356 4866				
	Fax: 319 356 7171				
	Email: paul.mccray@uiowa.edu				
	Tissue Procurement: Dr. M. J. Welsh, University of Iowa				
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Researchers may obtain clones from Research				
	Genetics (www.resgen.com) or from Open Biosystems				
	(www.openbiosystems.com).				

```

FEATURES
source
    . . 273
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="UI-CF-FNO-aeu-e-07-0-UI"
    /tissue_type="Human Lung Epithelial cells"
    /lab_host="PH108 (Life Technologies) (T1 phage resistant)"
    /clone_lib="UI-CF-FNO"
    /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
    modified polylinker; Site 1: Ecor I; Site 2: Not I;
    UI-CF-FNO is a subcloned cDNA library derived from two
    normalized Human lung epithelial cell libraries [EN1 and
    DUN]. The library was subcloned according to according to
    Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
    1996. For additional information, contact:
    bento-soares@uiowa.edu
    TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
    TAG_LIB=UI-CF-FNO

```


Db

497 TGCTGGTGTGCTGCACCATTAACCTCA 523

RESULT 56
BQ352132
LOCUS
DEFINITION IL3-HT0619-100700-208-A10 HT0619 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ352132
VERSION BQ352132.1 GI:21016188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-HT0619-100700-208-A10&t3=2000-07-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 226.

FEATURES
source -
1..226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0619"
/notes="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 14.0%; Score 98; DB 3; Length 226;
Best Local Similarity 91.2%; Pred. No. 2-2e-07;
Matches 104; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 TTTTCCTTTTTATTATTAATACTTTTAGGGTACATGCGAAAGTGTCAGTATACATATATACATGA 108
DB TTATTTTATTTTATTATTAATACTTTTAGGGTACATGCGAAAGTGTCAGTATACATATATACATGA 166
QY 109 GTTAGTTACATATATACATGCGCAGTGTGCTGCCACCCATTAACCTCA 162
DB |||||

RESULT 57
A0628311
LOCUS
DEFINITION CITBI-EI-2650L21.TF CITBI-EI Homo sapiens genomic clone 2650L21,
ACCESSION A0628311
VERSION A0628311.1 GI:5090703
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other GSSs: CITBI-EI-2650L21.TF
Contact: Shaving Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source -
1..480
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2650L21"
/sex="male"
/cell_type="sperm"
/clone_lib="CITBI-EI"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

ORIGIN
Query Match 14.0%; Score 98; DB 11; Length 480;
Best Local Similarity 82.7%; Pred. NO. 2.1e-07;
Matches 124; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 12 AAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTAT 71
DB ATATTTTATCTATTGTTTTTTTGTGAATTAATAATATTTGTTTTTATTTATTTATTTATTTAT 369
QY 72 ACTTTTAAGTTTTTAGGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGT 131
DB 370 ACTTT-AGTTTTAGGGTACATGTGCAAGTGTGCAGGTTAGTTACATATGTATACCTGT 428
QY 132 GCCATGCTGGTGTGCTGCACCATTAACTC 161
DB 429 GCCATGCTGGTGTGCTGCACCATTAACTC 458

RESULT 58
CR958489
LOCUS
DEFINITION CR958489 740 bp DNA linear GSS 07-JUN-2005
Homo sapiens PAC end sequence of RZPDB737G0315D from genomic library (orig. Pieter J. de Jong library RPCI-3), genomic survey sequence.

ACCESSION CR958489
VERSION CR958489.1 GI:66955830
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 740)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Schwarz, F., Neubert, P., Schneider, D., Peters, M. and Korn, B.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg, Germany

COMMENT RZPD; RZPDB737G0315D; RP3-416J7;
derived from Dieter J. de Jong library RPCI-3;
http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=RZPDB737G0315D
RZPDB1B; (Human Genomic Set - RZPD 1.0) RZPD LIB No.737
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=737
http://www.rzpd.de/products/genomicset/
Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone distribution: http://www.rzpd.de/products/genomicset/
Seq-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)
Class: BAC ends.

FEATURES
source Location/Qualifiers
1. .740
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RZPDB737G0315D"
/sex="Male"
/clone_lib="RPCI-3"
/note="Vector: pCYPAC2; RPCI-3 Human Male PAC Library"

ORIGIN
Query Match 14.0%; Score 98; DB 14; Length 740;
Best Local Similarity 80.4%; Pred. No. 2e-07;
Matches 127; Conservative 0; Mismatches 30; Indels 1; Gaps 1;
QY 4 TTTACATATAAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATT 63
DB 291 TTCATGTGAAGATTTGCTGCTTCTGCTATTACATATTTATTGTTCTTTTATT 350
QY 64 ATTATTATACCTTTTAAGTTTTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATAT 123
DB 351 ATTATTATAC-TTTAAGTTTTAGGTACATGTCGCAATGTCGAGGTAGTTACATATGT 409
QY 124 ATACATGTGCATGCTGCTGCTGCACCACTTAACCTC 161
DB 410 ATACATGTGCATGCTGCTGCTGCACCTCATTAACCTC 447

RESULT 59
B75832 385 bp DNA linear GSS 08-APR-1999
DEFINITION RPCI11-12116.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12116,
genomic survey sequence.
ACCESSION B75832
VERSION B75832.1 GI:2771519
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 385)
AUTHORS Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI11-12116.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdaams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1. .385
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7504431"
/db_xref="taxon:9606"
/clone="RPCI-11-12116"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN
Query Match 14.0%; Score 97.8; DB 11; Length 385;
Best Local Similarity 79.5%; Pred. No. 2.3e-07;
Matches 128; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 4 TTTACATATAAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATT 63
DB 173 TTAGAAAAGTGTTTTTTTTTTTTGTGTTTGAATTTGGCATTTTATAATTATT 232
QY 64 ATTATTATACCTTTTAAGTTTTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATAT 123
DB 233 ACTATTATAC-TTTAAGTTTTAGGTACGTCGACATGCGCAGGTAGTTACATATGT 291
QY 124 ATACATGTGCCATGCTGCTGCTGCACCACTTAACCTCACA 164
DB 292 ATACATGTGCCGTCGCTGCTGCACCACTTAACCTCAGA 332

RESULT 60
CR750736/c 657 bp mRNA linear EST 30-AUG-2004
LOCUS DKFp470L1122_r1 470 (synonym: pliv1) Pongo pygmaeus cDNA clone
DEFINITION DKFp470L1122 5', mRNA sequence.
ACCESSION CR750736
VERSION CR750736.1 GI:51669903
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
REFERENCE 1 (bases 1 to 657)
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
TITLE Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clon from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
ordering:
http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKFZp470L1122
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
Location/Qualifiers

Db 194 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTAGTACATATGTATACATGTGCGCA 253
 Qy 136 TCGTGGTGTGCTGCACCACTAAC 159
 Db 254 TCGTGGTGTGCTGCACCACTAAC 277

RESULT 63
 C2465237 708 bp DNA linear GSS 20-OCT-2005
 LOCUS MCF756k05TF Human MCF7 breast cancer cell line library (MCF7.1)
 DEFINITION Homo sapiens genomic clone MCF7_56k05, genomic survey sequence.
 ACCESSION C2465237
 VERSION 1
 KEYWORDS GSS.
 SOURCE C2465237.1 GI:77948426
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 708)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 TITLE Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
 JOURNAL Unpublished (2005)
 COMMENT Contact: Volik SV
 Colin Collins' lab
 UCSF Comprehensive Cancer Center
 UCSF Box 0808, San Francisco, CA 94143-0808, USA
 Tel: 415 502 7066
 Fax: 415 502 5665
 Email: svolik@cc.ucsf.edu
 This clone is available from Amplicon Express
 http://www.genomex.com
 Class: BAC ends.

FEATURES
 source 1..708
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="MCF7_56k05"
 /sex="female"
 /clone_lib="Human MCF7 breast cancer cell line library (MCF7.1)"
 /note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN
 Query Match 13.9%; Score 97.6; DB 13; Length 708;
 Best Local Similarity 77.6%; Pred. No. 2.4e-07;
 Matches 118; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 10 ATAAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTTTATTATTAT 69
 Db 136 ATCACTTATTCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 195
 Qy 70 ATACTTTTAAGTTTATAGGTACATGTGCACCACTAAC 129
 Db 196 TATACCTTTAAAGTTTATAGGTACATGTGCACCACTAAC 255
 Qy 130 GTGCCATGCTGGTGTGCTGCACCACTAAC 161
 Db 256 GTGCCATGCTGGTGTGCTGCACCACTAAC 287

RESULT 64
 C2465237 708 bp DNA linear GSS 20-OCT-2005
 LOCUS MCF756k05TF Human MCF7 breast cancer cell line library (MCF7.1)
 DEFINITION Homo sapiens genomic clone MCF7_56k05, genomic survey sequence.
 ACCESSION C2465237
 VERSION 1
 KEYWORDS GSS.
 SOURCE C2465237.1 GI:77948426
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 708)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 TITLE Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
 JOURNAL Unpublished (2005)
 COMMENT Contact: Volik SV
 Colin Collins' lab
 UCSF Comprehensive Cancer Center
 UCSF Box 0808, San Francisco, CA 94143-0808, USA
 Tel: 415 502 7066
 Fax: 415 502 5665
 Email: svolik@cc.ucsf.edu
 This clone is available from Amplicon Express
 http://www.genomex.com
 Class: BAC ends.

FEATURES
 source 1..708
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="MCF7_56k05"
 /sex="female"
 /clone_lib="Human MCF7 breast cancer cell line library (MCF7.1)"
 /note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN
 Query Match 13.9%; Score 97.6; DB 13; Length 708;
 Best Local Similarity 77.6%; Pred. No. 2.4e-07;
 Matches 118; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 10 ATAAAGTTTTTTTTTTTGTATGATTTTAAATAAATATCATTTCTTTTTTATTATTAT 69
 Db 136 ATCACTTATTCATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 195
 Qy 70 ATACTTTTAAGTTTATAGGTACATGTGCACCACTAAC 129
 Db 196 TATACCTTTAAAGTTTATAGGTACATGTGCACCACTAAC 255
 Qy 130 GTGCCATGCTGGTGTGCTGCACCACTAAC 161
 Db 256 GTGCCATGCTGGTGTGCTGCACCACTAAC 287

RESULT 65
 AG121371/c
 LOCUS AG121371
 DEFINITION Pan troglodytes DNA, clone: PTB-130G10.F, genomic survey sequence.
 ACCESSION AG121371
 VERSION AG121371.1 GI:16650536
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)

B72013
 LOCUS B72013
 DEFINITION B72013
 ACCESSION B72013
 VERSION B72013.1 GI:2711234
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 443)
 AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
 TITLE Use of BAC End Sequences for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other_GSSs: RPC111-7E20.TP
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..443
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GBB:7502419"
 /db_xref="taxon:9606"
 /clone="RPC1-11-7E20"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPC1-11"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPC111 Human Male BAC Library"

FEATURES
 source 1..443
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GBB:7502419"
 /db_xref="taxon:9606"
 /clone="RPC1-11-7E20"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPC1-11"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPC111 Human Male BAC Library"

ORIGIN
 Query Match 13.9%; Score 97.4; DB 11; Length 443;
 Best Local Similarity 78.9%; Pred. No. 2.7e-07;
 Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 75
 Db 260 TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 319

Qy 76 TTAAGTTTATAGGTACATGTGCACCACTAAC 162
 Db 320 TTAAGTTTATAGGTACATGTGCACCACTAAC 406

Qy 136 TCGTGGTGTGCTGCACCACTAAC 162
 Db 380 TCGTGGTGTGCTGCACCACTAAC 406

RESULT 65
 AG121371/c
 LOCUS AG121371
 DEFINITION Pan troglodytes DNA, clone: PTB-130G10.F, genomic survey sequence.
 ACCESSION AG121371
 VERSION AG121371.1 GI:16650536
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 661)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
FEATURES
source Location/Qualifiers
1..661
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130G10.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 13.9%; Score 97.4; DB 14; Length 661;
Best Local Similarity 78.9%; Pred. No. 2.6e-07;
Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 16 TTTTCTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACTT 75
Db 431 TTATTATTTTGTGCTCAAAACCAGTAATGCTTTCTTTTATTCTTTTATTATT 372
Qy 76 TTAAGTTTGTAGGTACATGTCACCAAGTGTGAGGTAGTTACATATATATACATGCGCA 135
Db 371 TTAAGTTTGTAGGTACATGTCACCAAGTGTGAGGTAGTTACATATATATACATGCGCA 312
Qy 136 TGCTGGTGTGCTGCACCACTTAACCTCA 162
Db 311 TGTTGGTGTGCTGCACCACTTAACCTCA 285
RESULT 66
CZ179389/c 712 bp DNA linear GSS 31-JAN-2005
LOCUS AC105347Chiol_tcl00.b1 Chimpanzee genomic DNA Pan troglodytes
DEFINITION genomic, genomic survey sequence.
ACCESSION CZ179389
VERSION CZ179389.1 GI:58347682
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE
AUTHORS 1 (bases 1 to 712)
Hillier, L.W., Graves, T.A., Fulton, R.S., Fulton, L.A., Pepin, K.H.,
Minx, P., Wagner-McPherson, C., Layman, D., Wyllie, K., Sekhon, M.,
Becker, M.C., Fowell, G.A., Delehaanty, K.D., Miner, T.L., Nash, W.E.,
Kremetzki, C., Oddy, L., Du, H., Sun, H., Bradshaw-Cordum, H., Ali, J.,

Carter, J., Cordes, M., Harris, A., Isak, A., van Brunt, A., Nguyen, C.,
Du, F., Courtney, L., Kalicki, J., Ozersky, P., Abbott, S.,
Armstrong, J., Belter, E.A., Caruso, L., Cedroni, M., Cotton, M.,
Davidson, J., Desai, A., Elliott, G., Erb, T., Fronick, C., Gaige, T.,
Haakenson, W., Haglund, K., Holmes, A., Harkins, R., Kim, K.,
Kruchowski, S., Strong, C.M., Grewal, N., Goyea, E., Hou, S., Levy, A.,
Martinka, S., Mead, K., McLellan, M.D., Meyer, R., Randall-Maher, J.,
Tomlinson, C., Dauphin-Kohlberg, S. et al.
Generation and annotation of the DNA sequences of human chromosomes
2 and 4
JOURNAL Nature 434 (7034), 724-731 (2005)
PUBMED 15815621
COMMENT Contact: Joanne Nelson
Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, St. Louis, MO 63108, USA
Tel: (314)286-1839
Fax: (314)286-1810
Email: submissions@watson.wustl.edu
Class: PCR with specific primers.
FEATURES
source Location/Qualifiers
1..712
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone_lib="Chimpanzee genomic DNA"
ORIGIN
Query Match 13.9%; Score 97.4; DB 13; Length 712;
Best Local Similarity 78.9%; Pred. No. 2.6e-07;
Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 15 GTTCTTTTCTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACTT 74
Db 693 GATTTTGTGAAAGAAAGAAATTTAAAGGATTTATTCCTTTTTTTTAAATATACC 634
Qy 75 TTTAAGTTTGTAGGTACATGTCACCAAGTGTGAGGTAGTTACATATATATACATGTCGC 134
Db 633 TTTAAGTTTGTGAGGTACATGTCACATTTGTCAGTTTAGTTACATATATATACATGTCGC 574
Qy 135 ATGCTGGTGTGTCGCCACCACTTAACCTC 161
Db 573 ATGCTGGTGTGTCGCCACCACTTAACCTC 547
RESULT 67
BZ610242 725 bp DNA linear GSS 08-JUN-2003
LOCUS WHADR41TF Human MCF7 breast cancer cell line library (MCF7.1) Homo
DEFINITION sapiens genomic clone MCF7.1-23G10, genomic survey sequence.
ACCESSION BZ610242
VERSION BZ610242.1 GI:31518803
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 725)
Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,
Gray, J.W. and Collins, C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
JOURNAL 12789976
PUBMED Contact: Volik SV
COMMENT Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express

ORIGIN

```
Query Match      13.9%; Score 97.4; DB 6; Length 995;
Best Local Similarity 87.4%; Pred.No. 2.5e-07;
Matches 118; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
```

QY Db	27 TGAATGTTTAAATAAATCATCTTCCTTTTTATTATTAACACTTTTAGTTAGTTTAG 86 490 TTATGAAAAAAAATAATTTTTTCCTTTTTTTTATATATATATATAC-TTTAAGTTTTAG 548
QY Db	87 GGATACATGTGCCAAGTGCGAGTTAGTTACATATATATACATGCCTCCATGGTGGTGTC 146 549 GGATACATGTGCCAATGTGCAGGTAGTTACATATGTATACATGTGCCATGCTGGTGGC 608
QY Db	147 TGCACCCTAACCTC 161 609 TGCACCCCTAACCTC 623

RESULT 69
BF954789/c

LOCUS BF954789 238 bp mRNA linear EST 22-JAN-2001

DEFINITION PM3-NN1203=U51100-001-d08 NN1203 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF954789

VERSION BF954789.1 GI:12372064

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 238)
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

REFERENCE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

AUTHORS Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001

JOURNAL Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM3&t2=PM3-NN1203+1
151100-001-d08&t3=2000-11-15&t4=1)

PUBLISHED Seq primer: puc 18 forward
High quality sequence stop: 219.
Location/Qualifiers
1..238
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

COMMENTS /clone_lib="NN1203"
/notes="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source

ORIGIN

```
Query Match      13.9%; Score 97.2; DB 2; Length 238;
```

Best Local Similarity 83.6%; Pred. No. 3e-07; Mismatches 23; Indels 1; Gaps 1; Matches 122; Conservative 0;

QY 16 TTTTGTGATGATTTTAAATAAATACATTTCTTTTATTATTATTACTT 75
DB 187 TTTTGTGATGATTTTAAATAAATACATTTCTTTTATTATTATTACTT 128
QY 76 TTAAGTTTGGGTACATGTCACCAAGTGTGCAGGTTAGTTACATATATATACATGTC 135
DB 127 -TAAAGTTTGGGTACATGTCACCAAGTGTGCAGGTTAGTTACATATATATACATGTC 135
QY 136 TGCTGGTGTGTCACCACTAACTC 161
DB 68 GGCTGGTGTGTCACCACTAACTC 43

RESULT 70

AI570164 256 bp mRNA linear EST 13-MAY-1999
LOCUS to75f07.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2184133 3'
DEFINITION similar to contains L1.b1 L1 repetitive element ;, mRNA sequence.

ACCESSION AI570164
VERSION AI570164.1 GI:4533538
KEYWORDS EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 256)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center,
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 379 Std Error: 0.00
Seg primer: -40UP from Gibco
POLYA-No.

FEATURES Location/Qualifiers
1..256
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2184133"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN

Query Match 13.9%; Score 97.2; DB 1; Length 256;
Best Local Similarity 83.1%; Pred. No. 3e-07; Mismatches 23; Indels 2; Gaps 1; Matches 123; Conservative 0;

QY 16 TTTTGTGATGATTTTAAATAAATACATTTCTTTTATTATTATTACT- 74
DB 7 TTTTGTGATGATTTTAAATAAATACATTTCTTTTATTATTATTATA 66
QY 75 -TTTAAAGTTTGGGTACATGTCACCAAGTGTGCAGGTTAGTTACATATATACATGTC 133

Db 67 CTTTAAAGTTTGGGTACATGTCACCAATGTGCAGGTTTGTACATATGTATACATGTGC 126
QY 134 CATGCTGGTGTGCTGCACCCCACTTAATC 161
DB 127 CATGTTGGTGTGCTGCACCCCACTTAATC 154
Search completed: July 19, 2006, 09:20:55
Job time : 4416 secs

THIS PAGE BLANK (USPTO)